

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 15, 2004, 12:21:40 ; Search time 77.4088 Seconds
(without alignments)
1241.024 Million cell updates/sec

Title: US-10-021-121-4
Perfect score: 1850
Sequence: 1 MGPPHSGPGGVRVGALLLLG.....PVYIVQDGPPQSPPNIYYKV 340

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	1850	100.0	340	2	AAW31544	Aaw31544 Human cyt
2	1850	100.0	340	2	AAW33699	Aaw33699 AL-2-shor
3	1850	100.0	340	2	AAW10637	Aaw10637 NLERK2 li
4	1850	100.0	340	6	ABU07845	Abu07845 Human eph
5	1844	99.7	340	2	AAW17081	Aaw17081 EPH famil
6	1841	99.5	455	2	AAW33698	Aaw33698 AL-2-long
7	1836	99.2	340	2	AAW46615	Aaw46615 Human tra
8	1780	96.2	340	6	ABU07846	Abu07846 Mouse eph
9	637.5	34.5	334	2	AAW00287	Aaw00287 Mouse Eph

10	637.5	34.5	336	2	AAR92742	Aar92742	Murine he
11	635.5	34.4	336	6	ABU07844	Abu07844	Mouse eph
12	632	34.2	346	2	AAR55059	Aar55059	Elk tyros
13	632	34.2	346	2	AAR91930	Aar91930	Human cyt
14	632	34.2	346	2	AAW19249	Aaw19249	Human elk
15	632	34.2	346	2	AAW36055	Aaw36055	Human elk
16	632	34.2	346	2	AAW44323	Aaw44323	Human elk
17	632	34.2	346	6	ABU07841	Abu07841	Human eph
18	632	34.2	346	7	ABU62401	Abu62401	Human elk
19	631	34.1	346	2	AAR82606	Aar82606	Eph trans
20	630.5	34.1	331	2	AAW00288	Aaw00288	Chicken E
21	629.5	34.0	333	2	AAR94655	Aar94655	Ligand fo
22	629.5	34.0	333	2	AAR92743	Aar92743	Human hep
23	629.5	34.0	333	2	AAR89287	Aar89287	Human LER
24	629.5	34.0	333	2	AAW06337	Aaw06337	Full leng
25	629.5	34.0	333	2	AAW11308	Aaw11308	Receptor-
26	629.5	34.0	333	6	ABU07886	Abu07886	Novel hum
27	629.5	34.0	333	7	ADD89059	Add89059	TAT245. 1
28	619.5	33.5	308	2	AAR94656	Aar94656	Ligand fo
29	619.5	33.5	308	2	AAW06334	Aaw06334	Ligand #2
30	613.5	33.2	345	6	ABU07842	Abu07842	Mouse eph
31	492	26.6	89	3	AAY71438	Aay71438	Human eph
32	465	25.1	254	6	ABU07843	Abu07843	Human eph
33	453.5	24.5	658	3	AAY96782	Aay96782	Ephrin-B2
34	452.5	24.5	683	3	AAY96781	Aay96781	Ephrin-B1
35	447	24.2	229	5	AAE24019	Aae24019	Murine ep
36	443	23.9	229	5	AAE24020	Aae24020	Human eph
37	431.5	23.3	195	2	AAW06333	Aaw06333	Ligand #1
38	431.5	23.3	195	2	AAW11307	Aaw11307	Receptor-
39	284.5	15.4	92	4	AAM37671	Aam37671	Peptide #
40	284.5	15.4	92	5	ABG46524	Abg46524	Human pep
41	205.5	11.1	136	4	AAM37534	Aam37534	Peptide #
42	205.5	11.1	136	5	ABG46394	Abg46394	Human pep
43	204	11.0	82	3	AAY71437	Aay71437	Human eph
44	202.5	10.9	106	3	AAB54187	Aab54187	Human pan
45	201	10.9	82	3	AAY71436	Aay71436	Human eph

ALIGNMENTS

RESULT 1

AAW31544

ID AAW31544 standard; protein; 340 AA.

XX

AC AAW31544;

XX

DT 14-APR-1998 (first entry)

XX

DE Human cytokine Lerk-8.

XX

KW Lerk-8; cytokine; human; hek; elk; receptor tyrosine kinase; ligand;

KW neurodegenerative disease; wound healing; neovascularisation; diagnosis;

KW therapy.

XX

OS Homo sapiens.

XX

FH	Key	Location/Qualifiers
FT	Peptide	1. .27
FT		/label= Sig_peptide
FT	Protein	28. .340
FT		/label= Mat_protein
FT	Domain	28. .224
FT		/note= "extracellular domain"
FT	Modified-site	210. .212
FT		/note= "N-glycosylated"
FT	Domain	225. .251
FT		/note= "transmembrane domain"
FT	Domain	252. .340
FT		/note= "cytoplasmic domain"
FT	Misc-difference	325
FT		/note= "residue 325 is Leu in Lerk-8 variant"
XX		
PN	WO9736919-A2.	
XX		
PD	09-OCT-1997.	
XX		
PF	19-MAR-1997; 97WO-US004533.	
XX		
PR	21-MAR-1996; 96US-00621146.	
XX		
PA	(IMMV) IMMUNEX CORP.	
XX		
PI	Cerretti DP;	
XX		
DR	WPI; 1997-503043/46.	
DR	N-PSDB; AAT89519.	
XX		
PT	New isolated cytokine, Lerk-8 - binds to the hek and elk receptor	
PT	tyrosine kinases, used to develop products for diagnosis and therapy.	
XX		
PS	Claim 3; Page 32-33; 37pp; English.	
XX		
CC	This protein sequence comprises a novel human cytokine designated Lerk-8.	
CC	The amino acid sequence was deduced from a human foetal brain cDNA clone	
CC	(see AAT89519). Lerk-8 binds to the cell surface receptors hek and elk,	
CC	which are members of the eph/elk family of receptor tyrosine kinases.	
CC	Lerk-8 polypeptides, especially soluble polypeptides comprising amino	
CC	acid residues -27 to 142-197 of the full-length protein, can be expressed	
CC	in transformed host cells. These polypeptides can be used to purify hek	
CC	or elk proteins, and to purify or identify cells that express hek or elk	
CC	on the surface. Such cells can be used in various in vitro studies or in	
CC	vivo procedures, e.g. neural cells expressing elk can be administered to	
CC	a mammal afflicted with a neurodegenerative disorder. The Lerk-8	
CC	polypeptides can also be used to deliver diagnostic or therapeutic agents	
CC	to these cells (e.g. leukaemia cells). The Lerk-8 DNA and polypeptides	
CC	can also be used to: treat disorders mediated by defective or	
CC	insufficient amounts of Lerk-8; to treat disorders such as injury to	
CC	neural tissue or neurologic disease; to promote angiogenesis; and for	
CC	wound healing or stimulating neovascularisation of grafted tissues	
XX		
SQ	Sequence 340 AA;	

Query Match

100.0%; Score 1850; DB 2; Length 340;

Best Local Similarity 100.0%; Pred. No. 1.6e-142;
Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MGPPHSGPGGVRVGALLLLGLVGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MGPPHSGPGGVRVGALLLLGLVGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60

Qy     61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRDLRFTIKFQEY 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRDLRFTIKFQEY 120

Qy    121 SPNLWGHEFRSHHDYIIATSDGTREGLES LQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 SPNLWGHEFRSHHDYIIATSDGTREGLES LQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180

Qy    181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240

Qy    241 GVAGAGGAMCWRRRRRAKPSERHPGPGSFGRGGS LGLGGGGMGMPREAEPEGELGIALRGG 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GVAGAGGAMCWRRRRRAKPSERHPGPGSFGRGGS LGLGGGGMGMPREAEPEGELGIALRGG 300

Qy    301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYYKV 340
      ||||||||||||||||||||||||||||||||||||
Db    301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYYKV 340

```

RESULT 2

AAW33699

ID AAW33699 standard; protein; 340 AA.

XX

AC AAW33699;

XX

DT 30-APR-1998 (first entry)

XX

DE AL-2-short (AL-2s) protein.

XX

KW AL-2s; AL-2; AL-2-short; human; treatment; neurological disorder; tumour;
KW rheumatoid arthritis; wound healing; paralysis; angiogenesis; leukaemia;
KW psoriasis; Alzheimer's disease; epilepsy.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Peptide 1. .26

FT /note= "signal peptide"

FT Protein 27. .340

FT /note= "mature protein"

FT Domain 27. .219

FT /note= "extracellular domain"

FT Domain 220. .245

FT /note= "hydrophobic transmembrane domain"

XX

PN W09740153-A1.

XX

PD 30-OCT-1997.

Qy 121 SPNLWGHEFRSHHDYIIATSDGTREGLES LQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180
 |||
 Db 121 SPNLWGHEFRSHHDYIIATSDGTREGLES LQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180
 |||
 Qy 181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240
 |||
 Db 181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240
 |||
 Qy 241 GVAGAGGAMCWRRRRRAKPSES RHPGPGSFGRGGS LGLGGGGGMGPRAEAPGELGIALRGG 300
 |||
 Db 241 GVAGAGGAMCWRRRRRAKPSES RHPGPGSFGRGGS LGLGGGGGMGPRAEAPGELGIALRGG 300
 |||
 Qy 301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYYKV 340
 |||
 Db 301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYYKV 340
 |||

RESULT 3

AAW10637

ID AAW10637 standard; protein; 340 AA.

XX

AC AAW10637;

XX

DT 23-JUN-1997 (first entry)

XX

DE NLERK2 ligand for eph-related kinase.

XX

KW LERK; ligand for eph-related kinase; ERK; NLERK2;

KW receptor protein tyrosine kinase; cell proliferation;

KW cell differentiation; cell survival; nerve cell.

XX

OS Homo sapiens.

XX

FH	Key	Location/Qualifiers
----	-----	---------------------

FT	Peptide	1. .29
----	---------	--------

FT		/label= Sig_peptide
----	--	---------------------

FT	Protein	30. .340
----	---------	----------

FT		/label= Mat_protein
----	--	---------------------

FT	Modified-site	210
----	---------------	-----

FT		/label= N-glycosylation_site
----	--	------------------------------

FT	Domain	227. .251
----	--------	-----------

FT		/label= Transmembrane_domain
----	--	------------------------------

XX

PN WO9704091-A1.

XX

PD 06-FEB-1997.

XX

PF 19-JUL-1996; 96WO-AU000460.

XX

PR 20-JUL-1995; 95AU-00004263.

PR 27-NOV-1995; 95AU-00006847.

PR 22-DEC-1995; 95AU-00007299.

PR 05-FEB-1996; 96AU-00007890.

XX

PA (AMRA-) AMRAD OPERATIONS PTY LTD.

XX

PI Nicola NA;
 XX
 DR WPI; 1997-132632/12.
 DR N-PSDB; AAT60966.
 XX
 PT Nucleic acid mol. encoding ligand for eph-related kinase - useful for
 PT treatment of, pref. neuronal, cells to increase survival, proliferation
 PT and differentiation.
 XX
 PS Claim 16; Page 37-39; 7lpp; English.
 XX
 CC A novel human ligand for eph-related kinase (LERK) is designated NLERK2
 CC (AAW10637). It is encoded by a cDNA clone (AAT60966) obtd. from a human
 CC foetal brain cDNA library. The novel receptor ligand can be expressed in
 CC transformed host cells and used in methods for regulating the
 CC development, maintenance or regeneration of different cells (e.g.
 CC neurons) and tissues in vivo and in vitro. Soluble NLERK2 peptides can be
 CC used to treat injury, disease or abnormality in the nervous system, and
 CC membrane-bound NLERK2 to modulate proliferation, different or survival
 CC e.g. in grafting procedures or transplantation. NLERK2 can also be used
 CC to raise antibodies for use in immunotherapy, and to detect anti-NLERK2
 CC antibodies that may occur in some autoimmune diseases
 XX
 SQ Sequence 340 AA;

Query Match 100.0%; Score 1850; DB 2; Length 340;
 Best Local Similarity 100.0%; Pred. No. 1.6e-142;
 Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MGPPHSGPGGVRVGALLLLGLVGLVSGLSLEPVYWNSANKRFQAEAGGYVLYPQIGDRLDL	60
Db	1	MGPPHSGPGGVRVGALLLLGLVGLVSGLSLEPVYWNSANKRFQAEAGGYVLYPQIGDRLDL	60
Qy	61	LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRDLRFTIKFQEY	120
Db	61	LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRDLRFTIKFQEY	120
Qy	121	SPNLWGHEFRSHHDYIIATSDGTREGLESLOGGVCLTRGMKVLLRVGQSPRGGAVPRKP	180
Db	121	SPNLWGHEFRSHHDYIIATSDGTREGLESLOGGVCLTRGMKVLLRVGQSPRGGAVPRKP	180
Qy	181	VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL	240
Db	181	VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL	240
Qy	241	GVAGAGGAMCWRRRRRAKPSERHPGPGSFGRGGSGLGLGGGGMGPREAEPGELGIALRGG	300
Db	241	GVAGAGGAMCWRRRRRAKPSERHPGPGSFGRGGSGLGLGGGGMGPREAEPGELGIALRGG	300
Qy	301	GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPNNIYYKV	340
Db	301	GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPNNIYYKV	340

RESULT 4

ABU07845

ID ABU07845 standard; protein; 340 AA.

XX
 AC ABU07845;
 XX
 DT 10-MAY-2003 (first entry)
 XX
 DE Human ephrin-B3 ligand.
 XX
 KW Cytostatic; vasodilator; antiinflammatory; cardiant; gene therapy;
 KW ligand-receptor binding modulator; ephrin ligand; angiogenesis;
 KW lymphangiogenesis; aberrant Ephrin-Tie biology; cell growth disorder;
 KW cell migration disorder; cell proliferation disorder; neovascularisation;
 KW ischaemia; infarction; tissue graft; transplant; human; ephrin-B3;
 KW tie receptor tyrosine kinase; Eph receptor ligand.
 XX
 OS Homo sapiens.
 XX
 PN WO2003004529-A2.
 XX
 PD 16-JAN-2003.
 XX
 PF 02-JUL-2002; 2002WO-IB002524.
 XX
 PR 02-JUL-2001; 2001US-0302960P.
 XX
 PA (LICN) LICENTIA LTD.
 XX
 PI Alitalo K, Kubo H;
 XX
 DR WPI; 2003-210341/20.
 DR N-PSDB; ABX12546.
 XX
 PT Identifying modulators of binding between a Tie receptor tyrosine kinase
 PT and an Ephrin ligand, useful for promoting neovascularization, comprises
 PT contacting a Tie receptor with an Ephrin in the presence of a putative
 PT modulator.
 XX
 PS Disclosure; Page 117-119; 199pp; English.
 XX
 CC The invention describes a method of identifying a modulator of binding
 CC between a Tie receptor tyrosine kinase and an Ephrin ligand. The method
 CC comprises contacting a Tie receptor composition with an Ephrin
 CC composition in the presence and in the absence of a putative modulator
 CC compound, and detecting the binding between Tie receptor and the Ephrin
 CC in the presence and in the absence of the putative modulator. The method
 CC is useful for identifying a modulator of binding between a Tie receptor
 CC tyrosine kinase and an Ephrin ligand. Modulators identified from the
 CC method are useful in modulating angiogenic processes, including
 CC lymphangiogenesis, for treating diseases associated with aberrant Ephrin-
 CC Tie biology, aberrant growth, migration or proliferation of cells that
 CC express a Tie receptor, or for promoting growth of vessel or
 CC neovascularisation (e.g. ischaemic tissue, an infarction, a new or
 CC chronic compound, or a tissue graft or transplant). This is the amino
 CC acid sequence of human Ephrin-B3, a member of the Ephrin-B subclass of
 CC ligands that are bound to the membrane via a transmembrane domain and
 CC short cytoplasmic tail and function as Eph receptor ligands
 XX
 SQ Sequence 340 AA;

Query Match 100.0%; Score 1850; DB 6; Length 340;
 Best Local Similarity 100.0%; Pred. No. 1.6e-142;
 Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MGPPHSGPGGVRVGALLLLGLVGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60
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Db      1 MGPPHSGPGGVRVGALLLLGLVGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60

Qy     61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRDLRFTIKFQEY 120
      |||
Db     61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRDLRFTIKFQEY 120

Qy    121 SPNLWGHEFRSHHDYIIATSDGTREGLESQGQVCLTRGMKVLLRVGQSPRGGAVPRKP 180
      |||
Db    121 SPNLWGHEFRSHHDYIIATSDGTREGLESQGQVCLTRGMKVLLRVGQSPRGGAVPRKP 180

Qy    181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240
      |||
Db    181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240

Qy    241 GVAGAGGAMCWRRRRRAKPSERHPGPGSFGRGGSGLGLGGGGMGMPREAEFGELGIALRGG 300
      |||
Db    241 GVAGAGGAMCWRRRRRAKPSERHPGPGSFGRGGSGLGLGGGGMGMPREAEFGELGIALRGG 300

Qy    301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYYKV 340
      |||
Db    301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYYKV 340

```

RESULT 5

AAW17081

ID AAW17081 standard; protein; 340 AA.

XX

AC AAW17081;

XX

DT 09-AUG-1997 (first entry)

XX

DE EPH family ligand Efl-6.

XX

KW Efl-6; Eph; Elk; receptor tyrosine kinase; signal transduction; ligand;
 KW neurological disease.

XX

OS Homo sapiens.

XX

FH	Key	Location/Qualifiers
FT	Peptide	1. .24
FT		/label= Sig_peptide
FT	Protein	25. .340
FT		/label= Mat_protein
FT	Misc-difference	166
FT		/label= Gln, Arg
FT	Domain	225. .249
FT		/label= Transmembrane_domain

XX

PN W09715667-A1.

XX

PD 01-MAY-1997.
 XX
 PF 25-OCT-1996; 96WO-US017201.
 XX
 PR 25-OCT-1995; 95US-0007015P.
 XX
 PA (REGE-) REGENERON PHARM INC.
 XX
 PI Davis S, Gale NW, Yancopoulos GD;
 XX
 DR WPI; 1997-259021/23.
 DR N-PSDB; AAT69808.
 XX
 PT New nucleic acid encoding Efl-6 ligand protein - used for promoting
 PT growth and proliferation of neuronal cells and in drug screening.
 XX
 PS Claim 2; Fig 1; 36pp; English.
 XX
 CC A novel ligand (AAW17081), designated Efl-6 (or Eph transmembrane
 CC tyrosine kinase family ligand 6), binds to the Elk, Nuk/Cek5, Hek2/Sek4,
 CC Htk and Sek1 receptors on cells. Its amino acid sequence was deduced from
 CC a human frontal cortex cDNA clone (AAT69808). Recombinant Elf-6,
 CC truncated soluble polypeptides comprising the extracellular domain of Elf
 CC -6, and Efl-6 ligandbodies comprising soluble Efl-6 and the Fc portion of
 CC IgG can be expressed in host cells. These can be used to support neuronal
 CC and other Eph receptor-bearing cell populations for treatment of
 CC neurological disorders, in drug screening and to raise diagnostic
 CC antibodies
 XX
 SQ Sequence 340 AA;

Query Match 99.7%; Score 1844; DB 2; Length 340;
 Best Local Similarity 99.7%; Pred. No. 4.8e-142;
 Matches 339; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL	60
Db	1	MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL	60
QY	61	LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY	120
Db	61	LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY	120
QY	121	SPNLWGHEFRSHHDYIIATSDGTREGLESQGQVCLTRGMKVLLRVGQSPRGGA VPRKP	180
Db	121	SPNLWGHEFRSHHDYIIATSDGTREGLESQGQVCLTRGMKVLLXVQSPRGGA VPRKP	180
QY	181	VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL	240
Db	181	VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL	240
QY	241	GVAGAGGAMCWRRRRRAKPSES RHPGPGSFGRGGS LGLGGGGMGPREAEPGELGIALRGG	300
Db	241	GVAGAGGAMCWRRRRRAKPSES RHPGPGSFGRGGS LGLGGGGMGPREAEPGELGIALRGG	300
QY	301	GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIIYKV	340

RESULT 6

AAW33698

ID AAW33698 standard; protein; 455 AA.

XX

AC AAW33698;

XX

DT 30-APR-1998 (first entry)

XX

DE AL-2-long (AL-2l) protein.

XX

KW AL-2l; AL-2; AL-2-long; human; treatment; neurological disorder; tumour;

KW rheumatoid arthritis; wound healing; paralysis; angiogenesis; leukaemia;

KW psoriasis; Alzheimer's disease; epilepsy.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Peptide 1. .26

FT /note= "signal peptide"

FT Protein 27. .455

FT /note= "mature protein"

FT Domain 27. .219

FT /note= "extracellular domain"

FT Domain 220. .245

FT /note= "hydrophobic transmembrane domain"

XX

PN WO9740153-A1.

XX

PD 30-OCT-1997.

XX

PF 17-APR-1997; 97WO-US006345.

XX

PR 19-APR-1996; 96US-00635130.

XX

PA (GETH) GENENTECH INC.

XX

PI Caras IW;

XX

DR WPI; 1997-535837/49.

DR N-PSDB; AAV06354.

XX

PT Human AL-2 neurotrophic factor and related DNA - used to develop products
PT for, e.g. treating neurologic disorders, angiogenesis disorders, tumours
PT or rheumatoid arthritis or for wound healing.

XX

PS Claim 20; Fig 1A-C; 86pp; English.

XX

CC This is a AL-2-long (AL-2l) protein. The AL-2 is a novel Eph-related
CC tyrosine kinase receptor ligand. AL-2 can be administered to patients in
CC whom the nervous system has been damaged by trauma, surgery, stroke,
CC ischaemia, infection, metabolic disease, nutritional deficiency,
CC malignancy, or toxic agents, to promote the survival or growth of
CC neurons. They can be used to treat motoneuron disorders such as
CC amyotrophic lateral sclerosis (Lou Gehrig's disease), Bell's palsy, and

CC various conditions involving spinal muscular atrophy, or paralysis. AL-2
 CC can be used to treat human neurodegenerative disorders, such as
 CC Alzheimer's disease, Parkinson's disease, epilepsy, demyelinating
 CC diseases such as multiple sclerosis, Huntingtons chorea, Down's syndrome,
 CC nerve deafness, Menier's disease, and other disorders of the cerebellum.
 CC AL-2 can be used as cognitive enhancer, to enhance learning particularly
 CC in dementias or trauma, since they can promote axonal outgrowth and
 CC synaptic plasticity, particularly of hippocampal neurons that express AL-
 CC 2 binding Eph-family receptors and cortical neurons that express AL-2. AL
 CC -2 can also be used for wound healing, i.e. accelerating
 CC neovascularisation of, e.g. burns and ulcers. The encoding nucleic acids
 CC are useful in preparing antibodies that specifically bind to the AL-2
 CC protein. The antibodies and the AL-2 antagonists are useful in diagnosing
 CC and treating various neuronal disorders. AL-2 antagonists can be used for
 CC modulating angiogenesis. They can also be used for the treatment of
 CC tumours, acute myeloid leukaemia (AML), chronic myeloid leukaemia (CML),
 CC myelodysplastic syndrome (MDS), diabetic retinopathy, neovascular
 CC glaucoma, psoriasis and rheumatoid arthritis
 XX
 SQ Sequence 455 AA;

Query Match 99.5%; Score 1841; DB 2; Length 455;
 Best Local Similarity 100.0%; Pred. No. 1.2e-141;
 Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MGPPHSGPGGVRVGALLLLGLVLGLVSGLSLEPVYWNSANKRFQAEAGGYVLYPQIGDRLDL	60
Db	1	MGPPHSGPGGVRVGALLLLGLVLGLVSGLSLEPVYWNSANKRFQAEAGGYVLYPQIGDRLDL	60
Qy	61	LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCCEAPPAPNLLLTCDRPLDLRFTIKFQEY	120
Db	61	LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCCEAPPAPNLLLTCDRPLDLRFTIKFQEY	120
Qy	121	SPNLWGHEFRSHHDYIIATSDGTREGLESQGGVCLTRGMKVLLRVGQSPRGGAVPRKP	180
Db	121	SPNLWGHEFRSHHDYIIATSDGTREGLESQGGVCLTRGMKVLLRVGQSPRGGAVPRKP	180
Qy	181	VSEMPMERDRGAAHSLEPGKENLPGDPTSNAISRGAEGPLPPPSMPAVAGAAGGLALLLL	240
Db	181	VSEMPMERDRGAAHSLEPGKENLPGDPTSNAISRGAEGPLPPPSMPAVAGAAGGLALLLL	240
Qy	241	GVAGAGGAMCWRRRRAKPSERHPGPGSFGRGGSGLGLGGGGMGPREAEPGELGIALRGG	300
Db	241	GVAGAGGAMCWRRRRAKPSERHPGPGSFGRGGSGLGLGGGGMGPREAEPGELGIALRGG	300
Qy	301	GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIIY	338
Db	301	GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIIY	338

RESULT 7
 AAW46615
 ID AAW46615 standard; protein; 340 AA.
 XX
 AC AAW46615;
 XX
 DT 06-JUL-1998 (first entry)

XX
 DE Human transmembrane ligand Elk-L3.
 XX
 KW Elk-L3; Elk-related receptor tyrosine kinase; transmembrane ligand;
 KW human; signal transduction; axonogenesis; nerve cell; neurone;
 KW Alzheimer's disease; Parkinson's disease; Huntingdon's disease;
 KW demyelination; multiple sclerosis; amyotrophic lateral sclerosis;
 KW nervous system infection; Wernicke's disease; trauma; ischaemia; stroke;
 KW nutritional polyneuropathy; progressive supranuclear palsy;
 KW Shy Drager's syndrome; multistem degeneration;
 KW olivo ponto cerebellar atrophy, peripheral nerve damage.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 166
 FT /label= Gln, Arg
 FT Domain 225. .249
 FT /note= "transmembrane domain"
 XX
 PN WO9801548-A1.
 XX
 PD 15-JAN-1998.
 XX
 PF 04-JUL-1997; 97WO-CA000473.
 XX
 PR 05-JUL-1996; 96US-0021272P.
 XX
 PA (MOUN) MOUNT SINAI HOSPITAL CORP.
 XX
 PI Holland S, Mbamalu G, Pawson T;
 XX
 DR WPI; 1998-101047/09.
 DR N-PSDB; AAV16097.
 XX
 PT Modulating transmembrane ligand for an Elk-related receptor tyrosine
 PT kinase - by formation of a complex between an oligomerised Elk-related
 PT receptor tyrosine kinase and a transmembrane ligand.
 XX
 PS Disclosure; Fig 5A; 40pp; English.
 XX
 CC This polypeptide comprises human Elk-L3, a transmembrane ligand of Elk-
 CC related receptor tyrosine kinase (ERRTK). A novel method of modulating
 CC the biological activity of, or for affecting a pathway regulated by, a
 CC transmembrane ligand for an ERRTK in a cell expressing the transmembrane
 CC ligand comprises forming a complex between a purified and isolated
 CC oligomerised ERRTK, or an isoform or an extracellular domain of the
 CC ERRTK, and the transmembrane ligand expressed on the cell. The complex
 CC can also be used for evaluating a substance for its ability to modulate
 CC the biological activity of a transmembrane ligand for an ERRTK, and to
 CC identify substances that affect or modulate a pathway regulated by a
 CC ERRTK. A purified and isolated oligomerised ERRTK can be used in the
 CC preparation of a medicament for modulating neuronal development or
 CC regeneration in a subject, or in a medicament for modulating axonogenesis
 CC in a subject (all claimed). The substances identified by the methods can
 CC be used to modulate axonogenesis, nerve cell interactions and
 CC regeneration, to treat diseases and conditions involving trauma and

CC injury to the nervous system, such as Alzheimer's disease, Parkinson's
CC disease, Huntingdon's disease, demyelinating diseases, such as multiple
CC sclerosis, amyotrophic lateral sclerosis, bacterial and viral infections
CC of the nervous system, deficiency diseases, such as Wernicke's disease
CC and nutritional polyneuropathy, progressive supranuclear palsy, Shy
CC Drager's syndrome, multistem degeneration and olivo ponto cerebellar
CC atrophy, peripheral nerve damage, trauma, and ischaemia resulting from
CC stroke

XX

SQ Sequence 340 AA;

Query Match 99.2%; Score 1836; DB 2; Length 340;

Best Local Similarity 99.4%; Pred. No. 2.2e-141;

Matches 338; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy      1 MGPPHSGPGGVRVGALLLLGLVGLVSGLSLEPVYWNSANKRFQAEAGGYVLYPQIGDRLDL 60
          |||
Db      1 MGPPHSGPGGVRVGALLLLGLVGLVSGLSLEPVYWNSANKRFQAEAGGYVLYPQIGDRLDL 60

Qy     61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRDLRFTIKFQEY 120
          |||
Db     61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRDLRFTIKFQEY 120

Qy    121 SPNLWGHEFRSHHDYIIATSDGTREGLES LQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180
          |||
Db    121 SPNLWGHEFRSHHDYIIATSDGTREGLES LQGGVCLTRGMKVLLXVGQSPRGGAVPRKP 180

Qy    181 VSEMPMERDRGAAHSLEPGKENLPGDPTS NATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240
          |||
Db    181 VSEMPMERDRGAAHSLEPGKENLPGDPTS NATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240

Qy    241 GVAGAGGAMCWRRRRRAKPSESRHPGPGSFGRGGS LGLGGGGMGMPREAE PGELGIALRGG 300
          |||
Db    241 GVAGAGGAMCWRRRRRAKPSESRHPGPGSFGRGGS LGLGGGGMGMPREAE PGELGIALRGG 300

Qy    301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPQNIYYKV 340
          |||
Db    301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPQNIYYKV 340
```

RESULT 8

ABU07846

ID ABU07846 standard; protein; 340 AA.

XX

AC ABU07846;

XX

DT 10-MAY-2003 (first entry)

XX

DE Mouse ephrin-B3 ligand.

XX

KW Cytostatic; vasodilator; antiinflammatory; cardiant; gene therapy;

KW ligand-receptor binding modulator; ephrin ligand; angiogenesis;

KW lymphangiogenesis; aberrant Ephrin-Tie biology; cell growth disorder;

KW cell migration disorder; cell proliferation disorder; neovascularisation;

KW ischaemia; infarction; tissue graft; transplant; mouse; ephrin-B3;

KW tie receptor tyrosine kinase; Eph receptor ligand.

XX

OS Mus musculus.
 XX
 PN WO2003004529-A2.
 XX
 PD 16-JAN-2003.
 XX
 PF 02-JUL-2002; 2002WO-IB002524.
 XX
 PR 02-JUL-2001; 2001US-0302960P.
 XX
 PA (LICN) LICENTIA LTD.
 XX
 PI Alitalo K, Kubo H;
 XX
 DR WPI; 2003-210341/20.
 DR N-PSDB; ABX12547.
 XX
 PT Identifying modulators of binding between a Tie receptor tyrosine kinase
 PT and an Ephrin ligand, useful for promoting neovascularization, comprises
 PT contacting a Tie receptor with an Ephrin in the presence of a putative
 PT modulator.
 XX
 PS Disclosure; Page 121-122; 199pp; English.
 XX
 CC The invention describes a method of identifying a modulator of binding
 CC between a Tie receptor tyrosine kinase and an Ephrin ligand. The method
 CC comprises contacting a Tie receptor composition with an Ephrin
 CC composition in the presence and in the absence of a putative modulator
 CC compound, and detecting the binding between Tie receptor and the Ephrin
 CC in the presence and in the absence of the putative modulator. The method
 CC is useful for identifying a modulator of binding between a Tie receptor
 CC tyrosine kinase and an Ephrin ligand. Modulators identified from the
 CC method are useful in modulating angiogenic processes, including
 CC lymphangiogenesis, for treating diseases associated with aberrant Ephrin-
 CC Tie biology, aberrant growth, migration or proliferation of cells that
 CC express a Tie receptor, or for promoting growth of vessel or
 CC neovascularisation (e.g. ischaemic tissue, an infarction, a new or
 CC chronic compound, or a tissue graft or transplant). This is the amino
 CC acid sequence of mouse Ephrin-B3, a member of the Ephrin-B subclass of
 CC ligands that are bound to the membrane via a transmembrane domain and
 CC short cytoplasmic tail and function as Eph receptor ligands
 XX
 SQ Sequence 340 AA;

Query Match 96.2%; Score 1780; DB 6; Length 340;
 Best Local Similarity 95.6%; Pred. No. 8e-137;
 Matches 325; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

Qy 1 MGPPHSGPGGVRVGALLLLGLVGLVSGLSLEFPVYWNSANKRFQAEAGGYVLYPQIGDRLDL 60
 || || |||||:||||||| |||||||||||||||||||||||||||||||||||||
 Db 1 MGAPHFGPGGVQVGALLLLGFAGLVSGLSLEFPVYWNSANKRFQAEAGGYVLYPQIGDRLDL 60
 Qy 61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRC EAPPAPNLLLTCDRPDLDLRFITIKFQEY 120
 |||||||||||||:||||||| |||||||||||||||||||||||||||||||||||||
 Db 61 LCPRARPPGPHSSPSYEFYKLYLVEGAQGRRC EAPPAPNLLLTCDRPDLDLRFITIKFQEY 120
 Qy 121 SPNLWGHEFRSHHDYIIATSDGTREGLES LQGGVCLTRGMKVLLRVGQSPRGGA VPRKP 180

Db	121	SPNLWGHEFRSHHDYIIATSDGTREGLES LQGGVCLTRGMKVLLRVGQSPRGGAVPRKP	180
Qy	181	VSEMPMERDRGAHAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL	240
Db	181	VSEMPMERDRGAHAHSAEPGRDITPGDPSSNATSRGAEGPLPPPSMPAVAGAAGGMALLLL	240
Qy	241	GVAGAGGAMCWRRRRRAKPSES RHPGPGSFGRGGS LGLGGGGMGPREAEPGELGIALRGG	300
Db	241	GVAGAGGAMCWRRRRRAKPSES RHPGPGSFGRGGS LGLGGGGMGPREAEPGELGIALRGG	300
Qy	301	GAADPPFCPHYEKVSGDYGHVPYIVQDGPPQSPPNIYYKV	340
Db	301	GTADPPFCPHYEKVSGDYGHVPYIVQDGPPQSPPNIYYKV	340

RESULT 9

AAW00287

ID AAW00287 standard; protein; 334 AA.

XX

AC AAW00287;

XX

DT 19-JAN-1997 (first entry)

XX

DE Mouse Eph receptor ligand ELF-2.

XX

KW Eph receptor; ligand; ELF-2; tyrosine kinase; signal transduction;
KW organogenesis; oncogenesis; tumour; neurological disorder; diagnosis;
KW gene therapy.

XX

OS Mus sp.

XX

FH	Key	Location/Qualifiers
----	-----	---------------------

FT Domain

1. .224

FT /label=

/label= Extracellular domain

FT	Binding-site	31.	.155
----	--------------	-----	------

31. .155

FT /label= Receptor_binding_site

```
/label= Receptor binding site
```

FT Domain 226. .251

226. .251

FT /label= Transmembrane domain

```
/label= Transmembrane domain
```

XX

PN WO9626958-A2.

XX

PD 06-SEP-1996.

XX

PF 23-FEB-1996; 96WO-US002673.

XX

PR 27-FEB-1995; 95US-00395415.

XX

PA (HARD) HARVARD COLLEGE.

XX

PI Flanagan JG, Bergemann AD;

XX

DR WPI; 1996-433391/43.

DR N-PSDB; AAT40230.

XX

PT Eph receptor ligand, ELF-2, and DNA encoding it - used to treat or
PT prevent neurological diseases, and to modulate binding of ELF-2 to Eph

OS Mus musculus.
 XX
 PN WO9602645-A2.
 XX
 PD 01-FEB-1996.
 XX
 PF 14-JUL-1995; 95WO-US008812.
 XX
 PR 20-JUL-1994; 94US-00277722.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Bennett BD, Matthews W;
 XX
 DR WPI; 1996-105907/11.
 DR N-PSDB; AAT16470.
 XX
 PT Ligand for the hepatoma trans-membrane kinase receptor - useful for
 PT stimulating and inhibiting cells carrying the receptor, e.g. for treating
 PT neuro-degenerative disease.
 XX
 PS Claim 5; Fig 1(A-D); 88pp; English.
 XX
 CC Mouse (AAT16470) and human (AAT16471) Htk ligand which bind to, and
 CC activate, the Htk receptor, have been identified in a variety of tissues
 CC using a soluble Htk-Fc fusion protein. The predicted mol.wt. of the
 CC murine Htk ligand protein following a signal peptide cleavage is 34 kD
 CC with an estimated pI of 8.9. The murine and human ligands show 96%
 CC homology at the amino acid level. The DNA is used to produce recombinant
 CC ligands; for tissue- specific typing (partic. as a marker for breast
 CC cancer) and as a marker for human chromosome 13. The ligands (partic. in
 CC soluble form) are used to activate the tyrosine kinase domain of the Htk
 CC receptor, i.e. to stimulate or inhibit growth, differentiation, and/or
 CC activation of cells contg. the receptor, e.g. treatment of
 CC neurodegenerative diseases, since they are strongly expressed in the
 CC cerebral cortex, hippocampus, striatum and cerebellum. The ligands are
 CC also useful as a control or standard in assays, for generation of
 CC antibodies, as a mol. wt. marker, for growth in vitro of Htk-receptor
 CC positive cells, as research agent, in screening, etc
 XX
 SQ Sequence 336 AA;

Query Match 34.5%; Score 637.5; DB 2; Length 336;
 Best Local Similarity 42.1%; Pred. No. 1.2e-43;
 Matches 139; Conservative 49; Mismatches 129; Indels 13; Gaps 5;

Qy 14 GALLLLGVLGLVSGLSLEPVYWN SANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSS 73
 | |::| : : ||:||||:| :| | |||||::|::|: :
 Db 17 GLLMVL CRTAISRSIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV 73
 Qy 74 PNYEFYKLYLVGGAQGRCEAPPAPNLLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH 133
 ||::|::| | || || | || |::| |||||::| ||| :
 Db 74 GQY EYKVMVDKQADRCTIKKENTPLN CARPDQDVKFTIKFQEFSPNLWGLEFQKNK 133
 Qy 134 DYYIIATSDGTREGLES LQGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR 190
 |||||::|::| ||:: :||| || ||:|::|| | | | :|
 Db 134 DYYIIISTNGSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSARNHGPTRRPELEAGTN 193

CC comprises contacting a Tie receptor composition with an Ephrin
 CC composition in the presence and in the absence of a putative modulator
 CC compound, and detecting the binding between Tie receptor and the Ephrin
 CC in the presence and in the absence of the putative modulator. The method
 CC is useful for identifying a modulator of binding between a Tie receptor
 CC tyrosine kinase and an Ephrin ligand. Modulators identified from the
 CC method are useful in modulating angiogenic processes, including
 CC lymphangiogenesis, for treating diseases associated with aberrant Ephrin-
 CC Tie biology, aberrant growth, migration or proliferation of cells that
 CC express a Tie receptor, or for promoting growth of vessel or
 CC neovascularisation (e.g. ischaemic tissue, an infarction, a new or
 CC chronic compound, or a tissue graft or transplant). This is the amino
 CC acid sequence of mouse Ephrin-B2, a member of the Ephrin-B subclass of
 CC ligands that are bound to the membrane via a transmembrane domain and
 CC short cytoplasmic tail and function as Eph receptor ligands

XX

SQ Sequence 336 AA;

Query Match 34.4%; Score 635.5; DB 6; Length 336;
 Best Local Similarity 41.7%; Pred. No. 1.7e-43;
 Matches 139; Conservative 49; Mismatches 126; Indels 19; Gaps 5;

Qy	14	GALLLLGLVLGLVSGLSLEPVYWNSANKRFQAEAGGYVLYPQIGDRLDLLCPRARPPGPHSS	73
		:: : : : : : : :: : :	
Db	17	GLLMVLCRTAISRSIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV	73
Qy	74	PNYEFYKLYLVGGAQGRRCCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHH	133
		: :: : :: : : : :	
Db	74	GQYEEYKVMVDKQADRCTIKKENTPLLNCARPDQDVKFTIKFQEFSPNLWGLEFQKNK	133
Qy	134	DYYIIATSDGTREGLESLOGGVCLTRGMKVLLRVGQ-----SPRGGAVPRKPVSEMPME	187
		: :: : ::: : : :: :	
Db	134	DYYIISTNGSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSTRNHGPTRRPELE---A	190
Qy	188	RDRGAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGG	247
		: : : : : : : : : :	
Db	191	GTNGRSSTTSPFVKPNPGSSTDGNSAGHSNNLLGSEVALFAGIASGCIIFIVIIITLVV	250
Qy	248	AMCWRRRRRAKPSESRHPGPGSFGRGSLGLGGGGMGPREAEPGELGIALRGGGAADPPF	307
		: : : : : : :	
Db	251	LLLKYRRHRKHSPQHTTTLSTLATPKRGGNN---NGSEPSDVIPLR---TADSVF	303
Qy	308	CPHYEKVSGDYGHPVYIVQDGPPQSPPNIYYKV	340
		: :	
Db	304	CPHYEKVSGDYGHPVYIVQEMPPQSPANIYYKV	336

RESULT 12

AAR55059

ID AAR55059 standard; protein; 346 AA.

XX

AC AAR55059;

XX

DT 25-MAR-2003 (revised)

DT 28-JAN-1995 (first entry)

XX

DE Elk tyrosine kinase receptor ligand.

XX
 KW Vectors; elk-L protein; elk; ligands; cell growth; differentiation.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1. .24
 FT /note= "signal peptide"
 FT Protein 25. .346
 FT /note= "mature elk-L protein"
 XX
 PN WO9411384-A1.
 XX
 PD 26-MAY-1994.
 XX
 PF 15-NOV-1993; 93WO-US010955.
 XX
 PR 13-NOV-1992; 92US-00977693.
 XX
 PA (IMMV) IMMUNEX CORP.
 XX
 PI Lyman S, Beckmann MP, Baum PR;
 XX
 DR WPI; 1994-183415/22.
 DR N-PSDB; AAQ65486.
 XX
 PT New DNA encoding ligand for elk tyrosine kinase receptor - also related
 PT polypeptides, vectors, antibodies and probes, useful e.g. in studying
 PT cell differentiation or growth.
 XX
 PS Claim 7; Page 30; 35pp; English.
 XX
 CC The sequence is that of the elk-L protein able to bind elk, a tyrosine
 CC kinase receptor. The DNA may be incorporated into vectors which can used
 CC to study the role of elk and its ligands in cell growth and
 CC differentiation. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 346 AA;

Query Match 34.2%; Score 632; DB 2; Length 346;
 Best Local Similarity 39.5%; Pred. No. 3.4e-43;
 Matches 145; Conservative 48; Mismatches 116; Indels 58; Gaps 9;

QY 8 PGGVRVGALLLLGVLGLVSGL-----SLEPVYWN SANKRFQAEGGYVLYPQIGDRLDLL 61
 || :| |: |: : | :||| |:| |:| : | :||:||||:|::
 Db 4 PGQRWL GKWL VAMVVWALCRLATPLAKNLEFVSWSSLNPKFLSGKGLVIYPKIGDKLDII 63
 QY 62 CPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRDLRLFTIKFQEYS 121
 |||| | ||:||||| | | ||:|:|:|:|: :|:|||||:|
 Db 64 CPRAEAGRP-----YEYKLYLVRPEQAAACSTVLDPNVLVTCNRPEQEIRFTIKFQEFS 118
 QY 122 PNLWGHEFRSHHDYIIATSDGTREGLES LQGGVCLTRGMKVLLRVGQSPRGGAVPRKPV 181
 || | |:| ||||| :|:|:| ||||: :||| || ||:|:|:| | :
 Db 119 PNYMGLEFKKHHDYITSTNGSLEGLNREGGVCRTRTMKIIMKVGQDPNAVTPQEQLTT 178
 QY 182 SEMP MERDRGAHSLE-PGKENLPGDPTS NATSRGAEGPLPPPSMPAVAGAAGGLA---- 236
 | | | : : || || : | | ||:|:| :

Db 179 SRPSKEADNTVKMATQAPGSRGSLGSDGKHETVNQEEKSGP-----GASGGSSGDPD 231
 Qy 237 -----LLLLGVAGAGGA-----MCWRRRRRAKPSES RHPGPGSFGRGGS LGL 277
 : | | | | : | : | | : : | : | |
 Db 232 GFFNSKVALFAAVGAGCVIFLLIIIFLTVLLLKLKRHRKHTQQ-----RAAALSL 282
 Qy 278 ----GGGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP 333
 | | | | | : : | | : : | | | | | | | | | | : | | | |
 Db 283 STLASPKGGSGTAGTEPSDIIIPLR---TTENNYCPHYEKVSGDYGHPVYIVQEMPPQSP 339
 Qy 334 PNIYYKV 340
 | | | | |
 Db 340 ANIYYKV 346

RESULT 13

AAR91930

ID AAR91930 standard; protein; 346 AA.

XX

AC AAR91930;

XX

DT 25-MAR-2003 (revised)

DT 11-DEC-1996 (first entry)

XX

DE Human cytokine elk-ligand (elk-L).

XX

KW Human; cytokine; elk-ligand; elk-L; tyrosine kinase receptor;

KW neurotrophic; neuroprotective; placenta; radiolabelled probe; treatment;

KW neural tissue; excito-toxicity; injury; disorder; neural culture reagent;

KW immunogenic fragment; antibody.

XX

OS Homo sapiens.

XX

FH	Key	Location/Qualifiers
----	-----	---------------------

FT	Peptide	1. .24
----	---------	--------

FT		/label= sig_peptide
----	--	---------------------

FT	Peptide	25. .346
----	---------	----------

FT		/label= mat_peptide
----	--	---------------------

XX

PN US5512457-A.

XX

PD 30-APR-1996.

XX

PF 15-MAR-1994; 94US-00213403.

XX

PR 13-NOV-1992; 92US-00977693.

XX

PA (IMMV) IMMUNEX CORP.

XX

PI Carpenter MK, Lyman S, Beckmann MP, Baum PR;

XX

DR WPI; 1996-229866/23.

DR N-PSDB; AAT28770.

XX

PT DNA coding for neurotrophic human elk ligand cytokine - useful as probe
 PT to isolate other elk ligand sequences.

XX

PS Claim 1; Col 27-30; 18pp; English.

XX

CC The present sequence is the human cytokine elk-ligand (elk-L), which
CC binds a member of the tyrosine kinase receptor family. Elk-L exhibits
CC neurotrophic and neuroprotective properties, and has a calculated mol.
CC wt. 35180 daltons and a pI of 9.006. The elk-L cDNA, isolated from a
CC human placental cDNA library, can be radiolabelled and used as a probe
CC for isolating other mammalian elk-L cDNA. Elk-L can be used to treat
CC neural tissue disorders, partic. excito-toxicity associated injuries or
CC disorders, and as a neural culture reagent, while immunogenic fragments
CC of elk-L can be used to generate specific anti-elk-L antibodies. (Updated
CC on 25-MAR-2003 to correct PF field.)

XX

SQ Sequence 346 AA;

Query Match 34.2%; Score 632; DB 2; Length 346;
Best Local Similarity 39.5%; Pred. No. 3.4e-43;
Matches 145; Conservative 48; Mismatches 116; Indels 58; Gaps 9;

```
Qy      8 PGGVRVGALLLLGVLGLVSGL-----SLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLL 61
      ||  :|  |:  |:  :  |      :|||  |:|  |:|  :  |  |:|:| |:|:| |:|:
Db      4 PGQRWLKGKWL VAMVWALCRLATPLAKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDII 63

Qy     62 CPRARPPGPHSSPNYEFYKLYLVGGAQGRRC EAPPAPNLLLTCDRPDLDLRF TIKFQEYS 121
      |||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db     64 CPRAEAGRP-----YEYYKLYLVRPEQAAACSTVLDPNVLVTCNRPEQEIRFTIKFQEFS 118

Qy    122 PNLWGHEFRSHHDYIIATSDGTREGLES LQGGVCLTRGMKVLLRVGQSPRGGA VPRKPV 181
      ||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db    119 PNYMGLEFKKHHDYITSTSNGLSLEGLNREGGVCRTRTMKIIMKVGQDPNAVTP EQLT 178

Qy    182 SEMP MERDRGA AHSLE-PGKENLPGDPTS NATSRGAEGPLPPPSMPA VAGAAGGLA---- 236
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db    179 SRPSKEADNTVKMATQAPGSRGSLGDS DGKHETVNQEEKSGP-----GASGGSSGDPD 231

Qy    237 -----LLLLGVAGAGGA-----MCWRRRRRAKPSES RHPGPGSFGRGGS LGL 277
      :  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db    232 GFFNSKVALFAAVGAGCVIFLLIIIFLTVLLLKLKRHRKHTQQ-----RAAALS L 282

Qy    278 ----GGGGMGPREAEPGELGIALRGGAADPPFC PHYEKVSGDYGHPVYIVQDGPPQSP 333
      ||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db    283 STLASPKGGSGTAGTEPSDIIPLR---TTENNYCPHYEKVSGDYGHPVYIVQEMP PQSP 339

Qy    334 PNIYYKV 340
      |||||
Db    340 ANIYYKV 346
```

RESULT 14

AAW19249

ID AAW19249 standard; protein; 346 AA.

XX

AC AAW19249;

XX

DT 25-MAR-2003 (revised)

DT 18-AUG-1997 (first entry)

XX

DE Human elk ligand protien.
 XX
 KW Human; elk; ligand; elk-L; cytokine; testing; measuring; purification;
 KW neuroprotection; treatment; diabetic; hereditary; nutritional;
 KW neuropathy; neurodegenerative disease; tissue culture.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1. .24
 FT /label= sig_peptide
 FT Peptide 25. .346
 FT /label= mat_peptide
 XX
 PN US5627267-A.
 XX
 PD 06-MAY-1997.
 XX
 PF 01-JUN-1995; 95US-00458077.
 XX
 PR 13-NOV-1992; 92US-00977693.
 PR 15-MAR-1994; 94US-00213403.
 XX
 PA (IMMV) IMMUNEX CORP.
 XX
 PI Beckmann MP, Lyman S, Baum PR;
 XX
 DR WPI; 1997-271366/24.
 DR N-PSDB; AAT69766.
 XX
 PT Human elk ligand protein - for diagnostic or therapeutic use, e.g. as
 PT neuro-protective agent.
 XX
 PS Claim 1; Col 29-32; 18pp; English.
 XX
 CC The present sequence is a human elk ligand (elk-L) protein, which binds
 CC elk, has a calculated molecular weight of 35180 and an isoelectric point
 CC of 9.006. Elk-L is a cytokine that can be used to test cells for elk
 CC expression, measure the biological activity of elk, purify elk by
 CC affinity chromatography and as a neuroprotective agent to treat diabetic,
 CC hereditary and nutritional neuropathies and neurodegenerative diseases.
 CC It may also be added to tissue cultures to prolong the life of neurons.
 CC The elk-L cDNA was isolated from a human placental cDNA library, and is
 CC present as a cDNA insert in the recombinant vector deposited in strain
 CC ATCC 69085. (Updated on 25-MAR-2003 to correct PF field.)
 XX
 SQ Sequence 346 AA;

Query Match 34.2%; Score 632; DB 2; Length 346;
 Best Local Similarity 39.5%; Pred. No. 3.4e-43;
 Matches 145; Conservative 48; Mismatches 116; Indels 58; Gaps 9;

QY 8 PGGVRVGALLLLGVLGLVSGL-----SLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLL 61
 || :| |: |: : | :||| |:| |:| :| |:|:|:|:|:|:
 Db 4 PGQRWLGKWL VAMVVWALCRLATPLAKNLEPVSWSLNPKF LSGKGLVIYPKIGDKLDII 63
 QY 62 CPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLRLFTIKFQEYS 121


```

      |||| | ||:|||| | | ||:||||: ||: |||||:|
Db      64 CPRAEAGRP-----Y EYKLYLVRPEQAAACSTVLDPNVLVTCNRPEQEIRFTIKFQEF 118
QY      122 PNLWGHEFRSHHDYIIATSDGTREGLES LQGGVCLTRGMKVLLRVGQSPRGGAVPRKPV 181
      || | ||: ||||| :||:|: ||||: |||| | ||: |||| | :
Db      119 PNYMGLEFKKHHDYITSTSNGLSLEGLNREGGVCRTRTMKIIMKVGQDPNAVTPQLTT 178
QY      182 SEMPMERDRGAAHSLE-PGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLA---- 236
      | | | : : || | | : | | | ||: || :
Db      179 SRPSKEADNTVKMATQAPGSRGSLGSDGKHETVNQEEKSGP-----GASGGSSGDPD 231
QY      237 -----LLLLGVAGAGGA-----MCWRRRRRAKPSES RHPGPGSFGRGGS LGL 277
      : | || | : | | | : | : | : | : |
Db      232 GFFNSKVALFAAVGAGCVIFLLIIIFLTVLLKLKRHRKHTQQ-----RAAALSL 282
QY      278 ----GGGGMGPREAEPGELGIALRGGAADPPFCPHYEKVSGDYGHFVYIVQDGPPQSP 333
      || | || : : || | : : ||||| ||||| : |||||
Db      283 STLASPKGSGTAGTEPSDIIIPLR---TTENNYCPHYEKVSGDYGHFVYIVQEMPPQSP 339
QY      334 PNIYYKV 340
      |||||
Db      340 ANIYYKV 346

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RESULT 15

AAW36055

ID AAW36055 standard; protein; 346 AA.

XX

AC AAW36055;

XX

DT 06-MAR-1998 (first entry)

XX

DE Human elk-L protein.

XX

KW Human; elk-L; cytokine; ligand; tyrosine kinase receptor; fusion protein;
 KW extracellular domain; immunoglobulin; neurological disease.

XX

OS Homo sapiens.

XX

FH	Key	Location/Qualifiers
----	-----	---------------------

FT	Peptide	1. .24
----	---------	--------

FT		/note= "signal peptide"
----	--	-------------------------

FT	Protein	25. .346
----	---------	----------

FT		/note= "mature protein"
----	--	-------------------------

FT	Domain	25. .237
----	--------	----------

FT		/note= "extracellular domain; this region is used to generate a fusion protein with the Fc portion of the human immunoglobulin G1"
----	--	--

FT	Modified-site	139. .141
----	---------------	-----------

FT		/note= "Asn is N-glycosylated"
----	--	--------------------------------

FT	Domain	238. .265
----	--------	-----------

FT		/note= "transmembrane domain"
----	--	-------------------------------

FT	Domain	266. .346
----	--------	-----------

FT		/note= "intracellular domain"
----	--	-------------------------------

FT	Cleavage-site	266. .267
----	---------------	-----------

FT		/note= "KEX2 protease cleavage site"
----	--	--------------------------------------

FT	Cleavage-site	267. .268
----	---------------	-----------

FT /note= "KEX2 protease cleavage site"
 FT Cleavage-site 270. .271
 FT /note= "KEX2 protease cleavage site"
 XX
 PN US5670625-A.
 XX
 PD 23-SEP-1997.
 XX
 PF 02-JUN-1995; 95US-00460741.
 XX
 PR 13-NOV-1992; 92US-00977693.
 PR 15-MAR-1994; 94US-00213403.
 XX
 PA (IMMV) IMMUNEX CORP.
 XX
 PI Beckmann MP, Lyman S, Baum PR;
 XX
 DR WPI; 1997-479524/44.
 DR N-PSDB; AAT97976.
 XX
 PT Soluble fusion proteins of human elk-ligand and Fc immunoglobulin
 PT fragment - and their dimers and oligomers, useful as neuro-protectants
 PT and neurotrophic agents.
 XX
 PS Claim 1; Col 27-30; 18pp; English.
 XX
 CC This is the amino acid sequence of the human elk-L protein, a new
 CC cytokine that is the ligand for the elk tyrosine kinase receptor. The
 CC extracellular domain of the protein (amino acids 1-213) is used to
 CC generate a fusion protein comprising the Fc polypeptide of the human
 CC immunoglobulin G1 (extending from the hinge region to the C-terminus).
 CC The fusion protein (which has the same activities as the natural elk-L
 CC protein) has neuroprotective and neurotrophic activity so is potentially
 CC useful for treating a wide range of neurological diseases
 XX
 SQ Sequence 346 AA;

Query Match 34.2%; Score 632; DB 2; Length 346;
 Best Local Similarity 39.5%; Pred. No. 3.4e-43;
 Matches 145; Conservative 48; Mismatches 116; Indels 58; Gaps 9;

QY 8 PGGVRV GALLLLGLVGLVSGL-----SLEPVY WNSANKRFQAEGGYVLYPQIGDRLDLL 61
 || :| |: |: : | :||| |:| |:| : | |:|:|:|:|:|:
 Db 4 PGQRWL GKWL VAMVVWALCRLATPLAKNLEPVSWSL NPKFLSGKGLVIYPKIGDKLDII 63
 QY 62 CPRARPPGPHSSPNYEFYKLYLVGGAQGRRC EAPPAPNLLLTCRDPDLDRFTIKFQEYS 121
 |||| | | :|:|:|:| | | | :|:|:|:|:|:|:|:|:|:|:
 Db 64 CPRAEAGRP-----YEYYKLYLVRPEQAAACSTVLDPNVLVTCNRPEQEIRFTIKFQEFS 118
 QY 122 PNLWGHEFRSHHDYIIATSDGTREGLES LQGGVCLTRGMKVLLRVGQSPRGGA VPRKPV 181
 || | |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
 Db 119 PNYMGLEFKKHHDYITSTSNGLSLEGLNREGGVCRTRTMKIIMKVGQDPNAVTP EQLT 178
 QY 182 SEMP MERDRGA AHSLE-PGKENLPGDPTS NATSRGAEGPLPPPSMPA VAGAAGGLA---- 236
 | | | : : || || : | | | :|:|:|:
 Db 179 SRPSKEADNTVKMATQAPGSRGSLGSDGKHETVNQEEKSGP-----GASGGSSGDPD 231

```

Qy      237 -----LLLLGVAGAGGA-----MCWRRRRRAKPSESRHPGPGSFGRGGS LGL 277
          : |      |||      : | : | | : :      | : | |
Db      232 GFFNSKVALFAAVGAGCVIFLLIIIFLTVLLKLRKRHRKHTQQ-----RAAALSL 282
          || |      || : : | ||      : : ||||| ||||| : |||||
Qy      278 ----GGGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP 333
          || |      || : : | ||      : : ||||| ||||| : |||||
Db      283 STLASPKGSGTAGTEPSDIIIPLR--TTENNYCPHYEKVSGDYGHPVYIVQEMPPQSP 339
          |||||
Qy      334 PNIYYKV 340
          |||||
Db      340 ANIYYKV 346

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Search completed: September 15, 2004, 12:35:57
Job time : 78.4088 secs

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OM protein - protein search, using sw model

Run on: September 15, 2004, 12:32:56 ; Search time 20.5283 Seconds
(without alignments)
855.055 Million cell updates/sec

Title: US-10-021-121-4
Perfect score: 1850
Sequence: 1 MGPPHSGPGGVRVGALLLG.....PVYIVQDGPPQSPENIYYKV 340

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
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6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	1846	99.8	340	4	US-09-214-631-3	Sequence 3, Appli
2	1844	99.7	340	4	US-09-051-994-2	Sequence 2, Appli
3	637.5	34.5	336	1	US-08-436-044-2	Sequence 2, Appli
4	637.5	34.5	336	2	US-08-436-054-2	Sequence 2, Appli
5	637.5	34.5	336	5	PCT-US95-08812-2	Sequence 2, Appli
6	632	34.2	346	1	US-08-213-403-2	Sequence 2, Appli
7	632	34.2	346	1	US-08-458-077-2	Sequence 2, Appli
8	632	34.2	346	1	US-08-460-741-2	Sequence 2, Appli
9	632	34.2	346	1	US-08-747-240-2	Sequence 2, Appli
10	632	34.2	346	1	US-08-299-567-6	Sequence 6, Appli
11	632	34.2	346	4	US-09-039-642B-2	Sequence 2, Appli

12	629.5	34.0	333	1	US-08-436-044-4	Sequence 4, Appli
13	629.5	34.0	333	2	US-08-436-054-4	Sequence 4, Appli
14	629.5	34.0	333	4	US-08-271-948-2	Sequence 2, Appli
15	629.5	34.0	333	4	US-08-739-333-2	Sequence 2, Appli
16	629.5	34.0	333	4	US-09-754-105-2	Sequence 2, Appli
17	629.5	34.0	333	4	US-09-978-339-2	Sequence 2, Appli
18	629.5	34.0	333	5	PCT-US95-08534-2	Sequence 2, Appli
19	629.5	34.0	333	5	PCT-US95-08812-4	Sequence 4, Appli
20	622.5	33.6	333	4	US-09-214-631-4	Sequence 4, Appli
21	608.5	32.9	345	4	US-09-214-631-5	Sequence 5, Appli
22	498	26.9	89	4	US-09-214-631-13	Sequence 13, Appl
23	201	10.9	82	4	US-09-214-631-11	Sequence 11, Appl
24	200.5	10.8	82	4	US-09-214-631-12	Sequence 12, Appl
25	179	9.7	234	1	US-08-299-567-5	Sequence 5, Appli
26	179	9.7	238	1	US-08-240-124-2	Sequence 2, Appli
27	179	9.7	238	1	US-08-453-943-2	Sequence 2, Appli
28	179	9.7	238	2	US-09-057-121-2	Sequence 2, Appli
29	179	9.7	238	3	US-09-358-734-2	Sequence 2, Appli
30	176.5	9.5	135	1	US-08-299-567-7	Sequence 7, Appli
31	176	9.5	184	1	US-09-609-324A-2	Sequence 2, Appli
32	176	9.5	184	2	US-08-920-440B-2	Sequence 2, Appli
33	176	9.5	184	3	US-09-173-492-2	Sequence 2, Appli
34	176	9.5	184	3	US-09-173-133-2	Sequence 2, Appli
35	176	9.5	184	3	US-09-165-533-2	Sequence 2, Appli
36	176	9.5	184	4	US-09-580-236A-2	Sequence 2, Appli
37	176	9.5	184	5	PCT-US95-12779-2	Sequence 2, Appli
38	176	9.5	184	5	PCT-US95-15781-2	Sequence 2, Appli
39	176	9.5	209	1	US-08-455-001-2	Sequence 2, Appli
40	176	9.5	209	3	US-08-308-814-2	Sequence 2, Appli
41	176	9.5	209	5	PCT-US95-11869-2	Sequence 2, Appli
42	175.5	9.5	213	1	US-09-609-324A-10	Sequence 10, Appl
43	175.5	9.5	213	2	US-08-920-440B-10	Sequence 10, Appl
44	175.5	9.5	213	3	US-09-173-492-10	Sequence 10, Appl
45	175.5	9.5	213	3	US-09-173-133-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1

US-09-214-631-3

; Sequence 3, Application US/09214631

; Patent No. 6413730

; GENERAL INFORMATION:

; APPLICANT: Holland, Sacha

; APPLICANT: Mbamalu, Geraldine

; APPLICANT: Pawson, Tony

; TITLE OF INVENTION: OLIGOMERIZED RECEPTORS WHICH AFFECT PATHWAYS REGULATED

; TITLE OF INVENTION: BY TRANSMEMBRANE LIGANDS FOR ELK-RELATED RECEPTOR

; TITLE OF INVENTION: TYROSINE KINASES

; FILE REFERENCE: 11757.23USWO

; CURRENT APPLICATION NUMBER: US/09/214,631

; CURRENT FILING DATE: 1999-03-12

; EARLIER APPLICATION NUMBER: PCT/CA97/00473

; EARLIER FILING DATE: 1997-07-04

; EARLIER APPLICATION NUMBER: 60/021,272

; EARLIER FILING DATE: 1996-07-05

; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 3
 ; LENGTH: 340
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-214-631-3

Query Match 99.8%; Score 1846; DB 4; Length 340;
 Best Local Similarity 99.7%; Pred. No. 2.2e-146;
 Matches 339; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEAGGYVLYPQIGDRDL 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEAGGYVLYPQIGDRDL 60

Qy     61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRDLRFTIKFQEY 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRDLRFTIKFQEY 120

Qy    121 SPNLWGHEFRSHHDYIIATSDGTREGLESIQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180
        ||||||||||||||||||||||||||||||||||||||||||||:|||||||
Db    121 SPNLWGHEFRSHHDYIIATSDGTREGLESIQGGVCLTRGMKVLLQVGQSPRGGAVPRKP 180

Qy    181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240
        ||||||||||||||||||||||||||||||||||||||||||||
Db    181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240

Qy    241 GVAGAGGAMCWRRRRRAKPSERHPGPGSFGRGGSGLGLGGGGMGPREAEPGELGIALRGG 300
        ||||||||||||||||||||||||||||||||||||||||||||
Db    241 GVAGAGGAMCWRRRRRAKPSERHPGPGSFGRGGSGLGLGGGGMGPREAEPGELGIALRGG 300

Qy    301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPQSPPNIIYKV 340
        ||||||||||||||||||||||||||||||||||||
Db    301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPQSPPNIIYKV 340
  
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RESULT 2

US-09-051-994-2

; Sequence 2, Application US/09051994A
 ; Patent No. 6602683
 ; GENERAL INFORMATION:
 ; APPLICANT: REGENERON PHARMACEUTICALS, INC.
 ; TITLE OF INVENTION: BIOLOGICALLY ACTIVE EPH FAMILY LIGANDS
 ; FILE REFERENCE: REG-341-PCT-US
 ; CURRENT APPLICATION NUMBER: US/09/051,994A
 ; CURRENT FILING DATE: 1998-04-24
 ; EARLIER APPLICATION NUMBER: PCT/US96/17201
 ; EARLIER FILING DATE: 1996-10-25
 ; EARLIER APPLICATION NUMBER: 60/007,015
 ; EARLIER FILING DATE: 1995-10-25
 ; NUMBER OF SEQ ID NOS: 3
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 2
 ; LENGTH: 340
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens


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; APPLICATION NUMBER: US/08/436,044
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/277722
; FILING DATE: 20-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 00,000
; REFERENCE/DOCKET NUMBER: 902D3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 336 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-436-044-2

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Query Match          34.5%; Score 637.5; DB 1; Length 336;
Best Local Similarity 42.1%; Pred. No. 1.7e-45;
Matches 139; Conservative 49; Mismatches 129; Indels 13; Gaps 5;

```

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Qy      14 GALLLLGLVGLVSGLSLEPVYWNSANKRFQAEAGGYVLYPQIGDRLDLLCPRARPPGPHSS 73
      | |::| : : |||:||||:| :| | | | | | | | | | | | : :
Db      17 GLLMVLCRTAISRSIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV 73

Qy      74 PNYEFYKLYLVGGAQGRRCAPPAPNLLLTCDRDLRFTIKFQEYSPNLWGHEFRSHH 133
      ||::|::| | | | | | | | | | | | | | | | | | | | | : :
Db      74 GQYEYKQVYMVDKQADRCTIKKENTPLLNCRPDQDVKFTIKFQEFSPNLWGLEFQKNK 133

Qy     134 DYYIIATSDGTREGLESQGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR 190
      ||||:|::|: |||::: |||| | | ||:|::|| | | | | :|
Db     134 DYYIISTSNGSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSARNHGPTRRPELEAGTN 193

Qy     191 GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC 250
      | : : | : | | | : : : | : | | | : : : : :
Db     194 GRSSTTSPFVKPNPGSSTDGNSAGHSGNLLGSEVALFAGIASGCIIFIVIIITLVVLLL 253

Qy     251 WRRRRRAKPSESRHPGPGSFGRGSLGLGGGGMGPREAEPGELGIALRGGGAADPPFCPH 310
      ||| : : | | : : | | : || : : | | | | | |
Db     254 KYRRRHRKHSPQHTTTLSLSTLATPKRGGNN---NGSEPSDVIIPLR---TADSVFCPH 306

Qy     311 YEKVS GDYGHVPVYIVQDGPPQSPNIIYKV 340
      ||||| | | | | | | | | | | | | | | | |
Db     307 YEKVS GDYGHVPVYIVQEMPPQSPANIIYKV 336

```

RESULT 4

US-08-436-054-2

```

; Sequence 2, Application US/08436054
; Patent No. 5864020
; GENERAL INFORMATION:
; APPLICANT: Bennett, Brian D.
; APPLICANT: Matthews, William

```



```

      ||| : :| | : || :|| :: || || |||
Db      254 KYRRRHRKHSPQHSTTSLSTLATPKRGNN----NGSEPSDVIPLR---TADSVFCPH 306

QY      311 YEKVSGDYGHPVYIVQDGPPQSPPNIYYKV 340
      ||||| : |||||
Db      307 YEKVSGDYGHPVYIVQEMPPQSPANIYYKV 336

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RESULT 5

PCT-US95-08812-2

; Sequence 2, Application PC/TUS9508812

; GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.

; TITLE OF INVENTION: HTK LIGAND

; NUMBER OF SEQUENCES: 7

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 460 Point San Bruno Blvd

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: patin (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US95/08812

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Lee, Wendy M.

; REGISTRATION NUMBER: 00,000

; REFERENCE/DOCKET NUMBER: 902PCT

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415/225-1994

; TELEFAX: 415/952-9881

; TELEX: 910/371-7168

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 336 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

PCT-US95-08812-2

Query Match 34.5%; Score 637.5; DB 5; Length 336;

Best Local Similarity 42.1%; Pred. No. 1.7e-45;

Matches 139; Conservative 49; Mismatches 129; Indels 13; Gaps 5;

QY 14 GALLLLGVLGLVSGLSLEPVYWNSANKRFQAEAGGYVLYPQIGDRLDLLCPRARPPGPHSS 73

Db 17 GLLMVLCRTAISRSIVLEPIYWSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV 73

Qy	74	PNYEFYKLYLVGGAQGRRC	EAPPAPNLLLTCDRPDL	DLRFTIKFQEYSPNLWGHEFRSHH	133
		: : : :		: : : :	
Db	74	GQYEEYKVMVDKDQADRCT	IKKENTPLLN	CARPDDVKFTIKFQEFSPNLWGLEFQKNK	133
Qy	134	DYYIIATSDGTREGLES	LQGGVCLTRGMKVLLRVGQ	--SPRGGA	VPRKPVSEMPMER-DR 190
		: : :	: :	:	
Db	134	DYYIISTSNGL	EGLDNQEGGVCQ	TRAMKILMKVGQDASSAGS	ARNHGPTRRPELEAGTN 193
Qy	191	GAASHLEPGKENLPGDPT	SNATSRGAEGPLPPPSMP	PAVAGAAGGLALLLLGVAGAGG	AMC 250
		: : :	: :	: : : : :	
Db	194	GRSSTTSPFVKPNPGS	STDGNSAGHSGNNLLGSE	VALFAGIASGCIIFIVIIITL	VLLL 253
Qy	251	WRRRRRAKPSES	RHPGPGSFGRGGS	LGLGGGGMGPREAEP	GELGIALRGGGAADPPFCPH 310
		: :	:	: : :	
Db	254	KYRRRHRKHSPQH	TTTSLSTLATPKRGGNN	---NGSEPSDVI	PLR---TADSVFCPH 306
Qy	311	YEKVS	GDYGH	PVYIVQDGPPQ	SPPNIYYKV 340
			:		
Db	307	YEKVS	GDYGH	PVYIVQEMPPQ	SPANIYYKV 336

; TELEFAX: (206) 233-0644
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 346 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-08-213-403-2

Query Match 34.2%; Score 632; DB 1; Length 346;
 Best Local Similarity 39.5%; Pred. No. 5e-45;
 Matches 145; Conservative 48; Mismatches 116; Indels 58; Gaps 9;

```

QY      8 PGGVRVGALLLLGLVGLVSGL-----SLEPVYWNSANKRFQAEGGYVLYPQIGDRDL 61
      ||  :| |: |: : | :||| |:| |:| : | |:|:|:|:|:|:|
Db      4 PGQRWLKWLVMVWALCRLATPLAKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDII 63

QY     62 CPRARPPGPHSSPNYEFYKLYLVGGAQGRRC EAPPAPNLLLTCDRPDLDLRF TIKFQEYS 121
      |||| | :|:|:|:|:| | | :|:|:|:|:| :|:|:|:|:|:|
Db     64 CPRAEAGRP-----YEYYKLYLVRPEQAAACSTVLDPNVLVTCNRPEQEIRFTIKFQEFS 118

QY    122 PNLWGHEFRSHHDYIIATSDGTREGLES LQGGVCLTRGMKVLLRVGQSPRGGA VPRKPV 181
      || | |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db    119 PNYMGLEFKKHHDYIITSTSNGLSLEGLNREGGVCRTRTMKIIMKVGD PNAVTPEQLTT 178

QY    182 SEMPMERDRGAAHSLE-PGKENLPGDPTS NATSRGAEGPLPPPSMPAVAGAAGGLA---- 236
      | | | : : || | | : | | | :|:|:|:|:|
Db    179 SRPSKEADNTVKMATQAPGSRGSLGDS DGKHETV NQEEKSGP-----GASGGSSGDPD 231

QY    237 -----LLLLGVAGAGGA-----MCWRRRRRAKPSES RHPGPGSFGRGGS LGL 277
      : | ||| : |:| | : : | :| |
Db    232 GFFNSKVALFAAVGAGCVIFLLIIIFLTVLLL KLRKRHRKH TQQ-----RAAALSL 282

QY    278 ----GGGGMGPREAEPGELGIALRGGGAADPPFC PHYEKVSGDYGHVPVYIVQDGPPQSP 333
      || | || : : || : :|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db    283 STLASPKGGSGTAGTEPSDIIIPLR---T TENNYCPHYEKVSGDYGHVPVYIVQEMPPQSP 339

QY    334 PNIYYKV 340
      |||||
Db    340 ANIYYKV 346
  
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RESULT 7

US-08-458-077-2

; Sequence 2, Application US/08458077
 ; Patent No. 5627267
 ; GENERAL INFORMATION:
 ; APPLICANT: Lyman, Stewart D.
 ; APPLICANT: Beckmann, M. Patricia
 ; APPLICANT: Baum, Peter R
 ; APPLICANT: Carpenter, Melissa
 ; TITLE OF INVENTION: No. 5627267el Cytokine Designated elk Ligand
 ; NUMBER OF SEQUENCES: 2
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Immunex Corporation
 ; STREET: 51 University Street
 ; CITY: Seattle

```

; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple System 7.1
; SOFTWARE: Microsoft Word for Apple, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,077
; FILING DATE: 01-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/213,403
; FILING DATE: 15-MAR-1994
; APPLICATION NUMBER: US 07/977,693
; FILING DATE: 13-NOV-1992
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2807-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 346 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-458-077-2

```

```

Query Match          34.2%; Score 632; DB 1; Length 346;
Best Local Similarity 39.5%; Pred. No. 5e-45;
Matches 145; Conservative 48; Mismatches 116; Indels 58; Gaps 9;

```

```

QY      8 PGGVRV GALLLLGVLGLVSGL-----SLEPVYWN SANKRFQAEGGYVLYPQIGDRDL 61
      ||  :|  |:  |:  :  |      :|||  |:|  |:|  :  |  |:|:|:|:|:|:|
Db      4 PGQRWL GKWL VAMVVWALCRLATPLAKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDII 63

QY     62 CPRARPPGPHSSPNYEFYKLYLVGGAQGRRC EAPPAPNLLLTCDRPDLRLFTIKFQEYS 121
      |||  |  |  ||:|:|:|  |  |  |  ||:|:|:|:|:|  :|:|:|:|:|:|
Db     64 CPRAEAGRP-----YEYKLYLV RPEQAAACSTVLDPNVLVTCNRPEQEIRFTIKFQEFS 118

QY    122 PNLWGHEFRSHHDYIIATSDGTREGLES LQGGVCLTRGMKVLLRVGQSPRGGA VPRKPV 181
      ||  |  ||:  |||:|  :|:|:|  |||:  :|:|  ||  ||:|:|:|  |  :
Db    119 PNYMGLEFKKHHDYIITSTSNGLSLEGLNREGGVCRTRTMKIIMKVGQDPNAV TPEQLTT 178

QY    182 SEMP MERDRGAHSL E-PGKENLPGDPTS NATSRGAEGPLPPPSMPAVAGAAGGLA----- 236
      |  |  |  :  :  ||  ||  :  |  |  |  ||:|:|  :
Db    179 SRPSKEADNTVKMATQAPGSRGSLGDS DGKHETVNQEEKSGP-----GASGGSSGDPD 231

QY    237 -----LLLLGVAGAGGA-----MCWRRRRRAKPSES RHPGPGSFGRGGSLGL 277
      :  |  |||  :  |:|  |  :  |  :|
Db    232 GFFNSKVALFAAVGAGCVIFLLIIIFLTVLL LKLRK RHRKHTQQ-----RAAALSL 282

```

Qy 278 ----GGGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP 333
 || | || :: | || : : ||||| : |||||
 Db 283 STLASPKGSGTAGTEPSDIIPLR---TTENNYCPHYEKVSGDYGHPVYIVQEMPQSP 339
 Qy 334 PNIYYKV 340
 |||||
 Db 340 ANIYYKV 346

RESULT 8

US-08-460-741-2
 ; Sequence 2, Application US/08460741
 ; Patent No. 5670625
 ; GENERAL INFORMATION:
 ; APPLICANT: Lyman, Stewart D.
 ; APPLICANT: Beckmann, M. Patricia
 ; APPLICANT: Baum, Peter R
 ; APPLICANT: Carpenter, Melissa
 ; TITLE OF INVENTION: No. 5670625el Cytokine Designated elk Ligand
 ; NUMBER OF SEQUENCES: 2
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Immunex Corporation
 ; STREET: 51 University Street
 ; CITY: Seattle
 ; STATE: Washington
 ; COUNTRY: USA
 ; ZIP: 98101
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: Apple Macintosh
 ; OPERATING SYSTEM: Apple System 7.1
 ; SOFTWARE: Microsoft Word for Apple, Version 5.1a
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/460,741
 ; FILING DATE: 02-JUN-1995
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/213,403
 ; FILING DATE: 15-MAR-1994
 ; APPLICATION NUMBER: US 07/977,693
 ; FILING DATE: 13-NOV-1992
 ; CLASSIFICATION: 530
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Seese, Kathryn A.
 ; REGISTRATION NUMBER: 32,172
 ; REFERENCE/DOCKET NUMBER: 2807-A
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (206) 587-0430
 ; TELEFAX: (206) 233-0644
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 346 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-08-460-741-2


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; APPLICATION NUMBER: US/08/747,240
; FILING DATE: 12-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/213,403
; FILING DATE: 15-MAR-1994
; APPLICATION NUMBER: US 07/977,693
; FILING DATE: 13-NOV-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2807-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 346 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-747-240-2

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```

Query Match          34.2%; Score 632; DB 1; Length 346;
Best Local Similarity 39.5%; Pred. No. 5e-45;
Matches 145; Conservative 48; Mismatches 116; Indels 58; Gaps 9;

```

```

Qy      8 PGGVRVGALLLLGVLGLVSGL-----SLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLL 61
      ||  :|  |:  |:  :  |      :|||  |:|  |  :|  :  |  |:|:|:|:|:|:|
Db      4 PGQRWLKGKWLAVMVVWALCRLATPLAKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDII 63

Qy     62 CPRARPPGPHSSPNYEFYKLYLVGGAQGRRCCEAPPAPNLLLTCDRPDLDLRFTIKFQEYS 121
      |||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db     64 CPRAEAGRP-----YEYKLYLVRPEQAAACSTVLDPNVLVTCNRPEQEIRFTIKFQEFS 118

Qy    122 PNLWGHEFRSHHDYIIATSDGTREGLESLOGGVCLTRGMKVLLRVGQSPRGGAVPRKPV 181
      ||  |  ||:  |||||  :||:|  |||:  :|||  ||  ||:|:|:|  |  :
Db    119 PNYMGLEFKKHHDYITSTSNGLSLEGLNREGGVCRTRTMKIIMKVGQDPNAVTPQLTT 178

Qy    182 SEMPMERDRGAHSLE-PGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLA---- 236
      |  |  |  :  :  ||  ||  :  |  |  |  |  |  |  |  |  |  |  |
Db    179 SRPSKEADNTVKMATQAPGSRGSLGSDGKHETVNQEEKSGP-----GASGGSSGDPD 231

Qy    237 -----LLLLGVAGAGGA-----MCWRRRRRAKPSESRRHPGPGSFGRGGSLLGL 277
      :  |  |||  :  |:|  |  :  :  |  |  |
Db    232 GFFNSKVALFAAVGAGCVIFLLIIIFLTVLLLLKLRKRHRKHTQQ-----RAAALSL 282

Qy    278 ----GGGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHVPVYIVQDGPPQSP 333
      ||  |  ||  :  :  ||  :  :  |||||  |||||  |||||  |||||
Db    283 STLASPKGSGTAGTEPSDIIPLR---TTENNYCPHYEKVSGDYGHVPVYIVQEMPQSP 339

Qy    334 PNIYYKV 340
      |||||
Db    340 ANIYYKV 346

```


RESULT 10
 US-08-299-567-6
 ; Sequence 6, Application US/08299567
 ; Patent No. 5747033
 ; GENERAL INFORMATION:
 ; APPLICANT: Davis, et al.
 ; TITLE OF INVENTION: METHOD OF ENHANCING THE BIOLOGICAL
 ; TITLE OF INVENTION: ACTIVITY OF EPH FAMILY LIGANDS
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Regeneron Pharmaceuticals, Inc.
 ; STREET: 777 Old Saw Mill River Road
 ; CITY: Tarrytown
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10591-6707
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/299,567
 ; FILING DATE: 01-SEP-1994
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Kempner, Gail M.
 ; REGISTRATION NUMBER: 32,143
 ; REFERENCE/DOCKET NUMBER: REG 290
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 914-345-7400
 ; TELEFAX: 914-345-7721
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 346 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: protein
 US-08-299-567-6

Query Match 34.2%; Score 632; DB 1; Length 346;
 Best Local Similarity 39.5%; Pred. No. 5e-45;
 Matches 145; Conservative 48; Mismatches 116; Indels 58; Gaps 9;

QY	8	PGGVRV GALLLLGVLGLVSGL-----SLEPVY WNSANKRFQAEGGYVLYPQIGDRLLD	61
		: : : : : : : : : : : ::	
Db	4	PGQRWL GKWL VAMVWALCRLATPLAKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDII	63
QY	62	CPRARPPGPHSSPNYEFYKLYLVGGAQGRRC EAPPAPNLLLTCDRPDLRLFTIKFQEYS	121
		: : : : : : : : : : :	
Db	64	CPRAEAGRP-----YEYKLYLVRPEQAAACSTVLDPNVLVTCNRPEQEIRFTIKFQEFS	118
QY	122	PNLWGHEFRSHHDYIIATSDGTREGLES LQGGVCLTRGMKVLLRVGQSPRGGA VPRKPV	181
		: : : : : : : : : : : : : : : : :	
Db	119	PNYMGLEFKKHHDYITSTSNGLSLEGLNREGGVCRTRTMKIIMKVGQDPNAVTPQLTT	178

Qy 182 SEMPMERDRGAAHSLE-PGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLA---- 236
 | | | : : | | | : | | : : : :
 Db 179 SRPSKEADNTVKMATQAPGSRGSLGSDGKHETVNQEEKSGP-----GASGGSSGDPD 231
 Qy 237 -----LLLLGVAGAGGA-----MCWRRRRRAKPSERHPGPGSFGRGGSGLGL 277
 : | | | : | : | : : | : |
 Db 232 GFFNSKVALFAAVGAGCVIFLLIIIFLTVLLKLKRHRKHTQQ-----RAAALSL 282
 Qy 278 ----GGGGMGPREAEPGELGIALRGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP 333
 | | | | : : | | : : | | | | | | | | | | : | | |
 Db 283 STLASPKGSGTAGTEPSDIIPLR---TTENNYCPHYEKVSGDYGHPVYIVQEMPPQSP 339
 Qy 334 PNIYYKV 340
 | | | |
 Db 340 ANIYYKV 346

RESULT 11

US-09-039-642B-2

; Sequence 2, Application US/09039642B

; Patent No. 6540992

; GENERAL INFORMATION:

; APPLICANT: Lyman, Stewart D.

; APPLICANT: Beckmann, M. Patricia

; APPLICANT: Baum, Peter R.

; APPLICANT: Carpenter, Melissa K.

; TITLE OF INVENTION: NOVEL CYTOKINE DESIGNATED ELK LIGAND

; FILE REFERENCE: GENENT.67CPDV3

; CURRENT APPLICATION NUMBER: US/09/039,642B

; CURRENT FILING DATE: 1998-03-16

; PRIOR APPLICATION NUMBER: 08/213,403

; PRIOR FILING DATE: 1994-03-15

; PRIOR APPLICATION NUMBER: 07/977,693

; PRIOR FILING DATE: 1992-11-13

; PRIOR APPLICATION NUMBER: 08/747,240

; PRIOR FILING DATE: 1996-10-12

; PRIOR APPLICATION NUMBER: 08/460,741

; PRIOR FILING DATE: 1995-06-02

; NUMBER OF SEQ ID NOS: 5

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 2

; LENGTH: 346

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-039-642B-2

Query Match 34.2%; Score 632; DB 4; Length 346;

Best Local Similarity 39.5%; Pred. No. 5e-45;

Matches 145; Conservative 48; Mismatches 116; Indels 58; Gaps 9;

Qy 8 PGGVRVGALLLLGVLGLVSGL-----SLEPVYWNSANKRFQAEGGYVLYPQIGDRDL 61
 | | : | : : : | : | | : | : | : | : | : | : | : | : | : | :
 Db 4 PGQRWLKGWLVAMVVWALCRLATPLAKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDII 63
 Qy 62 CPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYS 121
 | | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
 Db 64 CPRAEAGRP-----YEYKLYLVRPEQAAACSTVLDPNVLVTCNRPEQEIRFTIKFQEFS 118


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;       TELEX:   910/371-7168
; INFORMATION FOR SEQ ID NO:   4:
;   SEQUENCE CHARACTERISTICS:
;       LENGTH:   333 amino acids
;       TYPE:     amino acid
;       TOPOLOGY: linear
US-08-436-044-4

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Qy      14 GALLLLGLVLGLVSLGLEPIVYWSANKRFQAEGGVLYPQIGDRLLDCPRARPPGPHSS 73
      | |::| : : |||:||||:| :| | |||||:|::||: :
Db      14 GVLMVLCRTAISKSIVLEPIYWNSSNSKFLPGQGVLVYPQIGDKLDIICPKV---DSKTV 70

Qy      74 PNYEFYKLYLVGGAQGRRC EAPPAPNLLLTCDRDLRLFTTIKFQEYSPNLWGHEFRSHH 133
      ||::||:|:| | || | | :|| |::| |||||:| |||| | |: :
Db      71 GQY EYYKVYMVDKDQADRCTIKKENTPLLNCAKPDQDIKF TIKFQEFSPNLWGLEFQKNK 130

Qy      134 DYYIIATSDGTTREGLES LQGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR 190
      |||||:|:|:|: |||:: :||| | | |::|:| || | | : | : |
Db      131 DYYIIISTSNGLSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSTRNKDPTRRPELEAGTN 190

Qy      191 GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC 250
      | : : | : || | : : : : : | | | : : : : :
Db      191 GRSSTTSPFVKPNPGSSTDGNSAGHSNNILGSEVALFAGIASGCIIFIVIIITLVLLL 250

Qy      251 WRRRRRAKPSES RHPGPGSFGRGGS LGLGGGGMGMPREAE PGELGIALRGGGAADPPFCPH 310
      ||| : :| | : | : | :|| : : | || || |||
Db      251 KYRRRRHRKHSPQH TTTLSLSTLATPKRSGNN---NGSEPSDIIPLR---TADSVFCPH 303

Qy      311 YEKVSGDYGHVPVYIVQDGPPQSPPNIYYKV 340
      ||||| ||||| ||||| : |||| | ||||
Db      304 YEKVSGDYGHVPVYIVQEMPPQSPANIYYKV 333

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RESULT 13

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; Sequence 4, Application US/08436054
; Patent No. 5864020
; GENERAL INFORMATION:
;   APPLICANT:  Bennett, Brian D.
;   APPLICANT:  Matthews, William
;   TITLE OF INVENTION:  HTK LIGAND
;   NUMBER OF SEQUENCES:  7
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  Genentech, Inc.
;     STREET:     460 Point San Bruno Blvd
;     CITY:       South San Francisco
;     STATE:      California
;     COUNTRY:    USA
;     ZIP:        94080
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
;     COMPUTER:     IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS

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;   SOFTWARE:  patin (Genentech)
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/08/436,054
;   FILING DATE:  05-MAY-1995
;   CLASSIFICATION:  435
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  08/277722
;   FILING DATE:  20-JUL-1994
;   ATTORNEY/AGENT INFORMATION:
;   NAME:  Lee, Wendy M.
;   REGISTRATION NUMBER:  00,000
;   REFERENCE/DOCKET NUMBER:  902D1
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  415/225-1994
;   TELEFAX:  415/952-9881
;   TELEX:  910/371-7168
;   INFORMATION FOR SEQ ID NO:  4:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:  333 amino acids
;   TYPE:  amino acid
;   TOPOLOGY:  linear
US-08-436-054-4

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```

Query Match          34.0%;  Score 629.5;  DB 2;  Length 333;
Best Local Similarity 40.9%;  Pred. No. 7.8e-45;
Matches 135;  Conservative 52;  Mismatches 130;  Indels 13;  Gaps 5;

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QY      14 GALLLLGLVGLVSGLSLEPVYWNSANKRFQAEAGGYVLYPQIGDRLDLLCPRARPPGPHSS 73
      | |::| : : |||:||||:| :| | |||||:|::|: :
Db      14 GVLMLVCRTAISKSIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV 70

QY      74 PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRDLRLRFTIKFQEYSPNLWGHEFRSHH 133
      ||::|:|:| | || || | :|| |::| |||||:| ||||| ||: :
Db      71 GQYEYYKVYMVVDKQADRCTIKKENTPLLNCAKPDQDIKFTIKFQEFSPNLWGLEFQKNK 130

QY     134 DYYIIATSDGTREGLESQGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR 190
      |||||:|:|:| ||::: |||| | |||:|:| || | : | :|
Db     131 DYYIIISTNGSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSTRNKDPTRRPELEAGTN 190

QY     191 GAAHSLEPGKENLPGDPTSNAISRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC 250
      | : : | : || | : : : : : : || | | : : :
Db     191 GRSSTTSPFVKPNPGSSSTDGNSAGHSGNNILGSEVALFAGIASGCIIFIVIIITLVVLLL 250

QY     251 WRRRRRAKPSESRHPGPGSFGRGGSLLGLGGGGMGPREAEPGELGIALRGGAADPPFCPH 310
      ||| : : | | : | : | : || : : | || || |||
Db     251 KYRRRRHRKHSPQHTTTLSLSTLATPKRSGNN----NGSEPSDIIIPLR---PADSVFCPH 303

QY     311 YEKVSGDYGHPVYIVQDGPPQSPPNIIYKV 340
      ||||| ||||| ||||| |||||
Db     304 YEKVSGDYGHPVYIVQEMPPQSPANIIYKV 333

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RESULT 14

US-08-271-948-2

; Sequence 2, Application US/08271948

; Patent No. 6303769

; GENERAL INFORMATION:

```

; APPLICANT: Cerretti, Douglas P.
; APPLICANT: Reddy, Pranhitha
; TITLE OF INVENTION: No. 6303769e1 Cytokine Designated Lerk-5
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.1
; SOFTWARE: Microsoft Word, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/271,948
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2823
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 333 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-271-948-2

```

```

Query Match          34.0%; Score 629.5; DB 4; Length 333;
Best Local Similarity 40.9%; Pred. No. 7.8e-45;
Matches 135; Conservative 52; Mismatches 130; Indels 13; Gaps 5;

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QY      14 GALLLLGVLGLVSGLSLEPVYWNANKRFQAEAGGYVLYPQIGDRLDLLCPRARPPGPHSS 73
      | |::| : : |||:||||:| :| | |||||:|::|: :
Db      14 GVLMLCRLTAISKIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV 70

QY      74 PNYEFYKLYLVGGAQGRRCAPPAPNLLLTCDRDLRLFTIKFQEYSPNLWGHEFRSHH 133
      ||::|:| | | || | :|| |::|:|||||:||||| ||: :
Db      71 GQYEYYKVYMDKQDQADRCTIKKENTPLLCAKPDQDIKFTIKFQEFSPNLWGLEFQKNK 130

QY     134 DYYIIATSDGTREGLESQGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR 190
      ||||:|::|: ||::: :||| || ||:|::||| | | : | :|
Db     131 DYYIISTNGSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSTRNKDPTRRPELEAGTN 190

QY     191 GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC 250
      | : : | : || | :: : : : : || | | : :: : :
Db     191 GRSSTTSPFVKPNPGSSDTGNSAGHSGNNILGSEVALFAGIASGCIIFIVIIITLVVLLL 250

QY     251 WRRRRRAKPSESRRHPGPGSFGRGGSGLGLGGGGMGMPREAEFGELGIALRGGGAADPPFCPH 310

```

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      ||| : :| | : | :|| :: || || |||
Db      251 KYRRHRKHSPOHTTTLSTLATPKRSGNN---NGSEPSDIIIPLR---TADSVFCPH 303
QY      311 YEKVSGDYGHPVYIVQDGPPQSPPNIYYKV 340
      |||||:|||||:|||||
Db      304 YEKVSGDYGHPVYIVQEMPPQSPANIYYKV 333

```

RESULT 15

US-08-739-333-2

; Sequence 2, Application US/08739333

; Patent No. 6479459

; GENERAL INFORMATION:

; APPLICANT: Cerretti, Douglas P.

; APPLICANT: Reddy, Pranhitha

; TITLE OF INVENTION: No. 6479459el Cytokine Designated Lerk-5

; NUMBER OF SEQUENCES: 3

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Immunex Corporation

; STREET: 51 University Street

; CITY: Seattle

; STATE: Washington

; COUNTRY: US

; ZIP: 98101

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Apple Macintosh

; OPERATING SYSTEM: Apple 7.1

; SOFTWARE: Microsoft Word, Version 5.1a

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/739,333

; FILING DATE: 29-OCT-1996

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/271,948

; FILING DATE: 08-JUL-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Seese, Kathryn A.

; REGISTRATION NUMBER: 32,172

; REFERENCE/DOCKET NUMBER: 2823

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (206) 587-0430

; TELEFAX: (206) 233-0644

; TELEX: 756822

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 333 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-739-333-2

Query Match 34.0%; Score 629.5; DB 4; Length 333;

Best Local Similarity 40.9%; Pred. No. 7.8e-45;

Matches 135; Conservative 52; Mismatches 130; Indels 13; Gaps 5;

QY 14 GALLLLGVLGLVSGLSLEPVYWSANKRFQAEAGGYVLYPQIGDRLDLLCPRARPPGPHSS 73

Db	14	GVLMLCRTAISKSIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV	70
Qy	74	PNYEFYKLYLVGGAQGRCEAPPAPNLLLTCDRDLRFTIKFQEYSPNLWGHEFRSHH	133
Db	71	GQYEEYKVYMVVDKDQADRCTIKKENTPLLNCAPDQDIKFTIKFQEFSPNLWGLEFQKNK	130
Qy	134	DYYIIATSDGTREGLESLOGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR	190
Db	131	DYYIIISTSNGLSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSTRNKDPTRRPELEAGTN	190
Qy	191	GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC	250
Db	191	GRSSTTSPFVKPNPGSSTDGNSAGHSGNNILGSEVALFAGIASGCIIFIVIIITLVVLLL	250
Qy	251	WRRRRRAKPSESRRHPGPGSFGRGGSGLGSGGGGMGPRAEPGELGIALRGGGAADPPFCPH	310
Db	251	KYRRRRHRKHSPQHNTTTLSTLATPKRSGNN----NGSEPSDIIIPLR---TADSVFCPH	303
Qy	311	YEKVSGDYGHPVYIVQDGPPQSPPNIYYKV	340
Db	304	YEKVSGDYGHPVYIVQEMPPQSPANIYYKV	333

Search completed: September 15, 2004, 12:41:04
Job time : 21.5283 secs

OM protein - protein search, using sw model

Run on: September 15, 2004, 12:30:30 ; Search time 22.239 Seconds
(without alignments)
1470.620 Million cell updates/sec

Title: US-10-021-121-4
Perfect score: 1850
Sequence: 1 MGPPHSGPGGVVRVGALLLG.....PVYIVQDGPPQSPPNIIYKV 340

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query		Match Length	DB	ID	Description
	Score	Match				
1	637.5	34.5	336	2	I49766	hepatoma transmemb
2	632	34.2	346	2	S46993	elk ligand - human
3	629.5	34.0	333	2	I84743	hepatoma transmemb
4	613.5	33.2	345	2	I48780	Stral/Eplg2 protei
5	608.5	32.9	345	2	I58406	LERK-2 - rat
6	214.5	11.6	237	2	T19914	hypothetical prote
7	179	9.7	238	2	I38849	LERK-3 - human
8	176	9.5	209	2	A54984	ELF-1 protein prec
9	175.5	9.5	213	2	JE0322	ephrin-A2 - human
10	170.5	9.2	228	2	A57084	repulsive axon gui
11	169.5	9.2	201	2	I38850	LERK-4 - human
12	167.5	9.1	228	2	I58170	LERK-7 precursor -
13	166	9.0	205	2	A36377	B61 protein precur

14	159	8.6	680	2	S31216	collagen alpha 1(X
15	154.5	8.4	1049	1	CGBO7S	collagen alpha 1(I
16	153.5	8.3	1670	1	CGHU3B	collagen alpha 3(I
17	151.5	8.2	301	2	B31219	collagen 2 - Caeno
18	149	8.1	325	2	T32248	hypothetical prote
19	149	8.1	569	2	S42886	collagen - silkwor
20	148.5	8.0	316	2	T20497	hypothetical prote
21	148	8.0	921	2	S42617	collagen alpha 1(I
22	146.5	7.9	1315	2	A56101	collagen alpha 1(X
23	146.5	7.9	1492	2	A40333	collagen alpha 1'(
24	146.5	7.9	1774	2	B56101	collagen alpha 1(X
25	146	7.9	675	2	S20819	collagen alpha 3(I
26	145.5	7.9	305	2	T20906	hypothetical prote
27	145	7.8	674	2	S13301	collagen alpha 1(X
28	145	7.8	931	2	S13580	collagen alpha 1(I
29	144.5	7.8	438	2	S53787	collagen alpha cha
30	144	7.8	1027	2	S28774	collagen alpha cha
31	143	7.7	1747	2	A54121	collagen alpha-4 c
32	142.5	7.7	743	1	S23779	collagen alpha 1(V
33	142.5	7.7	1496	1	CGHU2V	collagen alpha 2(V
34	142	7.7	744	2	S15435	collagen alpha 1(V
35	142	7.7	1029	1	S21369	collagen alpha 2(V
36	142	7.7	1763	2	S16366	collagen alpha 2(I
37	141.5	7.6	1466	1	CGHU7L	collagen alpha 1(I
38	141	7.6	319	2	T32250	hypothetical prote
39	141	7.6	744	1	A34246	collagen alpha 1(V
40	141	7.6	744	1	S23298	collagen alpha 1(V
41	140.5	7.6	305	2	T30165	hypothetical prote
42	140	7.6	304	2	T22482	hypothetical prote
43	140	7.6	680	1	CGHU1D	collagen alpha 1(X
44	139.5	7.5	210	2	B44984	collagen - nematod
45	139	7.5	940	2	JE0291	FB19 protein - hum

ALIGNMENTS

RESULT 1

I49766

hepatoma transmembrane kinase ligand - mouse

C;Species: Mus musculus (house mouse)

C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999

C;Accession: I49766

R;Bennett, B.D.; Zeigler, F.C.; Gu, Q.; Fendly, B.; Goddard, A.D.; Gillett, N.; Matthews, W.

Proc. Natl. Acad. Sci. U.S.A. 92, 1866-1870, 1995

A;Title: Molecular cloning of a ligand for the EPH-related receptor protein-tyrosine kinase Htk.

A;Reference number: I49766; MUID:95199254; PMID:7534404

A;Accession: I49766

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-336 <RES>

A;Cross-references: GB:L38847; NID:g769677; PIDN:AAC42052.1; PID:g769678

C;Genetics:

A;Gene: HTK


```

      |||| | ||:|||| | | ||:||||: ||: |||||:|
Db      64 CPRAEAGRP-----Y EYKLYLVRPEQAAACSTVLDPNVLVTCNRPEQEIRFTIKFQEF 118
QY      122 PNLWGHEFRSHHDYIIATSDGTREGLES LQGGVCLTRGMKVLLRVGQSPRGGAVPRKPV 181
      || | ||: ||||| ||:|: ||||: |||| | ||: |||| | |
Db      119 PNYMGLEFKKHHDYITSTNGSLEGLNREGGVCRTRTMKIIMKVGQDPNAVTPPEQLTT 178
QY      182 SEMP MERDRGAAHSLE-PGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLA---- 236
      | | | : : || || : | | | ||: || :
Db      179 SRPSKEADNTVKMATQAPGSRGSLGSDGKHETVNQEEKSGP-----GASGGSSGDPD 231
QY      237 -----LLLLGVAGAGGA-----MCWRRRRRAKPSERHPGPSFGRGSSLGL 277
      : | || | : | | | : | : | : | : |
Db      232 GFFNSKVALFAAVGAGCVIFLLIIIFLTVLLKLRKRHRKHTQQ-----RAAALSL 282
QY      278 ----GGGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP 333
      || | || : | || : ||||| ||||| ||||| |||||
Db      283 STLASPKGSGTAGTEPSDIIIPLR---TTENNYCPHYEKVSGDYGHPVYIVQEMPQSP 339
QY      334 PNIYYKV 340
      |||||
Db      340 ANIYYKV 346

```

RESULT 3

I84743

hepatoma transmembrane kinase ligand - human

C;Species: Homo sapiens (man)

C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 05-Nov-1999

C;Accession: I84743

R;Bennett, B.D.; Zeigler, F.C.; Gu, Q.; Fendly, B.; Goddard, A.D.; Gillett, N.; Matthews, W.

Proc. Natl. Acad. Sci. U.S.A. 92, 1866-1870, 1995

A;Title: Molecular cloning of a ligand for the EPH-related receptor protein-tyrosine kinase Htk.

A;Reference number: I49766; MUID:95199254; PMID:7534404

A;Accession: I84743

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-333 <RES>

A;Cross-references: GB:L38734; NID:g769675; PIDN:AAC41752.1; PID:g769676

C;Genetics:

A;Gene: GDB:EPLG5; LERK5

A;Cross-references: GDB:438338; OMIM:600527

A;Map position: 13q33-13q33

Query Match 34.0%; Score 629.5; DB 2; Length 333;

Best Local Similarity 40.9%; Pred. No. 6.4e-37;

Matches 135; Conservative 52; Mismatches 130; Indels 13; Gaps 5;

```

QY      14 GALLLLGVLGLVSGLSLEPVYWSANKRFQAEAGGYLYPQIGDRDLLCPRARPPGPHSS 73
      | |::| : : |||:||||: | : | |||||:|:|:|: |
Db      14 GVLMLCRTAISKSIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV 70
QY      74 PNYEFYKLYLVGGAQGRRC EAPPAPNLLLTCDRPDLRLFTIKFQEYSPNLWGHEFRSHH 133
      ||:|:|:| | || || | :|| ||:| |||||:| ||||| ||: |
Db      71 GQY EYKVMVDKQDADRCTIKKENTPLNCAKPDQDIKFTIKFQEFSPNLWGLEFQKNK 130

```

Qy 134 DYYIIATSDGTREGLESLOGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR 190
 |||||:|:|:|: |||: :||| || ||:|:| || | | : | :|
 Db 131 DYYIIISTSNGLSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSTRNKDPTRRPELEAGTN 190
 Qy 191 GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC 250
 | : : | : || | : : : : : || | | : : : : :
 Db 191 GRSSTTSPFVKPNPGSSTDGNSAGHSGNNILGSEVALFAGIASGCIIFIVIIITLVVLLL 250
 Qy 251 WRRRRRAKPSESRHPGPGSFGRGGSGLGLGGGGMGPREAEPGELGIALRGGGAADPPFCPH 310
 ||| : :| | : | : || : : | || || |||
 Db 251 KYRRRHRKHSPQHTTTLSLSTLATPKRSGNN---NGSEPSDIIIPLR---TADSVFCPH 303
 Qy 311 YEKVSGDYGHPVYIVQDGPPQSPPNIIYKV 340
 ||||| ||||| ||||| : |||| |||||
 Db 304 YEKVSGDYGHPVYIVQEMPPQSPANIIYKV 333

RESULT 4

I48780

Stral/Eplg2 protein - mouse

C;Species: Mus musculus (house mouse)

C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999

C;Accession: I48780; A55507; A55062; S52670

R;Bouillet, P.; Oulad-Abdelghani, M.; Vicaire, S.; Garnier, J.M.; Schuhbaur, B.; Dolle, P.; Chambon, P.

Dev. Biol. 170, 420-433, 1995

A;Title: Efficient cloning of cDNAs of retinoic acid-responsive genes in P19 embryonal carcinoma cells and characterization of a novel mouse gene, Stral (mouse LERK-2/Eplg2).

A;Reference number: I48780; MUID:95377533; PMID:7649373

A;Accession: I48780

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-345 <RES>

A;Cross-references: EMBL:Z48781; NID:g747858; PIDN:CAA88695.1; PID:g747859

R;Fletcher, F.A.; Renshaw, B.; Hollingsworth, T.; Baum, P.; Lyman, S.D.;

Jenkins, N.A.; Gilbert, D.J.; Copeland, N.G.; Davison, B.L.

Genomics 24, 127-132, 1994

A;Title: Genomic organization and chromosomal localization of mouse Eplg2, a gene encoding a binding protein for the receptor tyrosine kinase Elk.

A;Reference number: A55507; MUID:95203867; PMID:7896266

A;Accession: A55507

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-345 <FLE>

A;Cross-references: GB:U07598

R;Shao, H.; Lou, L.; Pandey, A.; Pasquale, E.B.; Dixit, V.M.

J. Biol. Chem. 269, 26606-26609, 1994

A;Title: cDNA cloning and characterization of a ligand for the Cek5 receptor protein-tyrosine kinase.

A;Reference number: A55062; MUID:95014510; PMID:7929389

A;Accession: A55062

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-89, 'T', 91-345 <SHA>

A;Cross-references: GB:U12983; NID:g575928; PIDN:AAA53231.1; PID:g575929

C;Genetics:
A;Gene: EPLG2

Query Match 33.2%; Score 613.5; DB 2; Length 345;
Best Local Similarity 38.2%; Pred. No. 8.7e-36;
Matches 138; Conservative 51; Mismatches 107; Indels 65; Gaps 10;

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Qy      15 ALLLLGVLGLVSGL--SLEPVYWNANKRFQAEAGGYVLYPQIGDRLDLLCPRARPPGPHS 72
      |::| : | : | :||| |:| | : | |::|::|::|::|::| |
Db      15 AMVVLTLCLATPLAKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDIICPRAEAGRP-- 72

Qy      73 SPNYEFYKLYLVGGAQGRCEAPPAPNLLLTCDRPDLRLRFTIKFQEYSPNLWGHEFRSH 132
      ||:||||| | | |::|::|::| :|||::|::| | ||: :
Db      73 ---YEYYKLYLVRPEQAAACSTVLDPNVLVTCNKPHEIRFTIKFQEFSPNYMGLEFKKY 129

Qy     133 HDYIIATSDGTREGLESLOGGVCLTRGMKVLLRVGQSPRGGA VPRKPVSEMPMERDRGA 192
      |||| :||::| ||::| :||| || ||:::| | | : : | :
Db     130 HDYITSTSNGLSLEGLNREGGVCRTRTMKIVMKVGQDP-NAVTPQLTTSRPSKESDNT 188

Qy     193 AHSLEPGKENLPGDPTSNATSRGAEGP-----LPPPSMPAVAGAAGG-----LA 236
      : : | ||::| | | | |
Db     189 VKT-----ATQAPGRGSQGDSDGKHETVNQEEKSGPGAGGGGSGDSDSFFNSK 236

Qy     237 LLLLG VAGAGGA-----MCWRRRRRAKPSERHPPGPGSFGRGGSLGL----GG 279
      : | || | : | | | : | | | : | |
Db     237 VALFAAVGAGCVIFLLIIIFLTVLLKLRKRHRKHTQQ-----RAAALSSTLASP 287

Qy     280 GGGMGPREAEPGELGIALRGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYYK 339
      || | || : : | | : : |||||::|::|::|::|::|::|::|
Db     288 KGGSGTAGTEPSDIIPLR---TTENNYCPHYEKVSGDYGHPVYIVQEMPPQSPANIYYK 344

Qy     340 V 340
      |
Db     345 V 345
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RESULT 5

I58406

LERK-2 - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1999

C;Accession: I58406

R;Fletcher, F.A.; Carpenter, M.; Shilling, H.; Baum, P.; Ziegler, S.; Gimpel, S.; Hollingsworth, T.; VandenBos, T.; Davison, B.L.; Lyman, S.D.; Beckmann, M.P. Oncogene 9, 3241-3248, 1994

A;Title: LERK-2, a ligand for the receptor tyrosine kinase ELK, is evolutionarily conserved and expressed in a developmentally regulated pattern.

A;Reference number: I58406; MUID:95022634; PMID:7936648

A;Accession: I58406

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-345 <RES>

A;Cross-references: EMBL:U07560; NID:g563118; PIDN:AAA53092.1; PID:g563119

C;Genetics:

A;Gene: Eplg2

Query Match 32.9%; Score 608.5; DB 2; Length 345;

Best Local Similarity 38.0%; Pred. No. 1.9e-35;
Matches 137; Conservative 52; Mismatches 107; Indels 65; Gaps 10;

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QY      15 ALLLLGVLGLVSGL--SLEPVYWNSANKRFQAEGGYVLYPQIGDRDL DLCPRARPPGPHS 72
      |::| : | : | : ||| | : | : | : | : ||| : ||| : ||| |
Db      15 AMVVLTLCLATPLAKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDIICPRAEAGRP-- 72

QY      73 SPNYEFYKLYLVGGAQGRRCAPPAPNLLLTCDRDLRLFTIKFQEYSPNLWGHEFRSH 132
      ||:||||| | | ||:|:|:| :||| |||:| | | | : :
Db      73 ---YEYYKLYLVRPEQAAACSTVLDPNVLVTCKNPQQEIRFTIKFQEFSPNYMGLEFKKY 129

QY     133 HDYYIIATSDGTREGLES LQGGVCLTRGMKVLLRVGQSPRGGA VPRKPVSEMPMERDRGA 192
      |||| :|:|: | ||| : ||| || ||:|:| | | : : | :
Db     130 HDYYITSTSNGLSLEGLNREGGVCRTRTMKIVMKVGQDP-NAVTPEQLTTSRPSKESDNT 188

QY     193 AHSLEPGKENLPGDPTSNATSRGAEGP-----LPPPSMPAVAGAAGG-----LA 236
      : : | ||:| | | | : |
Db     189 VKT-----ATQAPGRGSQGSDSGKHETVNQQEKSGPGAGGSGSGDTSFFNSK 236

QY     237 LLLLG VAGAGGA-----MCWRRRRRAKPSERHPGPGSFGRGGS LGL----GG 279
      : | || | : | | : : | : |
Db     237 VALFAAVGAGCVIFLLIIIFLTVLLKLKRHRKHTQQ-----RAAALS LSTLASP 287

QY     280 GGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIIYYK 339
      | | || : | || : : ||| ||| ||| ||| : ||| |||
Db     288 KGDSGTAGTEPSDIIIPLR---TTENNYCPHYEKVSGDYGHPVYIVQEMPPQSPANIYYK 344

QY     340 V 340
      |
Db     345 V 345
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RESULT 6

T19914

hypothetical protein C43F9.8 - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C;Accession: T19914

R;Mortimore, B.

submitted to the EMBL Data Library, November 1996

A;Reference number: Z19195

A;Accession: T19914

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-237 <WIL>

A;Cross-references: EMBL:Z82262; PIDN:CAB54195.1; GSPDB:GN00022; CESP:C43F9.8

A;Experimental source: clone C43F9

C;Genetics:

A;Gene: CESP:C43F9.8

A;Map position: 4

A;Introns: 32/2; 96/3; 214/1

Query Match 11.6%; Score 214.5; DB 2; Length 237;
Best Local Similarity 25.7%; Pred. No. 4.6e-08;

Matches 53; Conservative 41; Mismatches 83; Indels 29; Gaps 6;

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QY      11 VRVGALLLLGVLGLVS-GLSLEPVYWNSANKRFQAEG-GYVLYPQIGDRDL DLCPRARPP 68
```

```

      ::: :|| : : : : : | ||:| | :|| : ||||: : ||::
Db      1 MQIATFILLSLFFFIGWARKIPDINWISSNPIFDVSNTHDVISVHIGDRVSIRCPKSD 60
QY      69 GPHSSPNYEFYKLYLVGGAQGRRCCEAPPAPNLLLTCDRDLRLRFTIKFQEYSPNLWGHE 128
      | : :||:| : | : | : || : : | : :|| | |
Db      61 G-----KYEYSYIYMVSDEEYDHCFL-SKPRLVGACDNQTINASINIVFRSFTPTPGGFE 114
QY      129 FRSHHDYIIIA-----TSDGTREGLES LQGGVCLTRGMKVLLRVGQ 169
      | : :||:| : : |||| ||:: : ||: : ||: |||
Db      115 FQPGKNYFLISKSEVDALIIYETANQIFPGTSDGTLEGIDRKDGLCTAKQMKIKFEVGQ 174
QY      170 SPRGGAVPRKPVSEMPMERDRGAAHS 195
      || | : : : :|| | |
Db      175 DRRGIENPK--FAARTLKKDRDAEHS 198

```

RESULT 7

I38849

LERK-3 - human

C;Species: Homo sapiens (man)

C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 29-Sep-1999

C;Accession: I38849

R;Kozlosky, C.J.; Maraskovsky, E.; McGrew, J.T.; VandenBos, T.; Teepe, M.;
 Lyman, S.D.; Srinivasan, S.; Fletcher, F.A.; Gayle, R.B.
 Oncogene 10, 299-306, 1995

A;Title: Ligands for the receptor tyrosine kinases hek and elk: isolation of
 cDNAs encoding a family of proteins.

A;Reference number: I38849; MUID:95140419; PMID:7838529

A;Accession: I38849

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-238 <RES>

A;Cross-references: EMBL:U14187; NID:g642832; PIDN:AAC50078.1; PID:g642833

C;Genetics:

A;Gene: GDB:EPLG3

A;Cross-references: GDB:438336; OMIM:601381

A;Map position: 1q21-1q22

C;Superfamily: axon guidance signal protein

Query Match 9.7%; Score 179; DB 2; Length 238;

Best Local Similarity 28.4%; Pred. No. 1.4e-05;

Matches 65; Conservative 24; Mismatches 80; Indels 60; Gaps 12;

```

QY      7 GPGGVRVVGALLLLGVLGLVSGLSLEPVYWN SANKRFQAEGGYVLYPQIGDRLDLLCP--R 64
      ||| | | : | |||:|: : | || : : | ||: ||
Db      24 GPG-----GALG-----NRHAVYWNSSNQHLRRE-GYTVQVNVNDYLDIYCPHYN 67
QY      65 ARPPGPHSSP----NYEFYKLYLVGGAQGRRCCEAPPAPNLLLTCDRDL---DLRFTIKF 117
      : || : | | ||:| | | | :|| :||: ||
Db      68 SSGVGPAGPGPGGGAEQYVLYMVSRNGYRTCNASQGFK-RWECNRPHAPHSPIKFSEKF 126
QY      118 QEYSPNLWGHEFRSHHDYIIATSDGTREGLES LQGGVCLTRGMKVLLRVGQSPRGGAVP 177
      | || | :|| : | :|| | : | || | : : |
Db      127 QRYSAFSLGYEFHAGHEYYYYISTPTHNLH-----WKCLR--MKVFVCCASTSHSG--- 174
QY      178 RKPVSEMP-----MERDRGAAHSLE-----PGKENLP 204
      ||| :| | : || | :|||

```


RESULT 8

A54984

ELF-1 protein precursor - mouse

N;Alternate names: Cek7 ligand

C;Species: Mus musculus (house mouse)

C;Date: 11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change 29-Sep-1999

C;Accession: A54984; A55873

R;Cheng, H.J.; Flanagan, J.G.

Cell 79, 157-168, 1994

A;Title: Identification and cloning of ELF-1, a developmentally expressed ligand for the Mek4 and Sek receptor tyrosine kinases.

A;Reference number: A54984; MUID:95007776; PMID:7522971

A;Accession: A54984

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-209 <CHE>

A;Cross-references: GB:U14941; NID:g558836; PIDN:AAA53636.1; PID:g558837

R;Shao, H.; Lou, L.; Pandey, A.; Verderame, M.F.; Siever, D.A.; Dixit, V.M. J. Biol. Chem. 270, 3467-3470, 1995

A;Title: cDNA cloning and characterization of a Cek7 receptor protein-tyrosine kinase ligand that is identical to the ligand (ELF-1) for the Mek-4 and Sek receptor protein-tyrosine kinases.

A;Reference number: A55873; MUID:95181289; PMID:7876076

A;Accession: A55873

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-209 <SHA>

A;Cross-references: GB:U14752; NID:g681886; PIDN:AAA68520.1; PID:g681887

C;Superfamily: axon guidance signal protein

C;Keywords: lipoprotein; membrane protein

Query Match 9.5%; Score 176; DB 2; Length 209;

Best Local Similarity 29.3%; Pred. No. 2e-05;

Matches 58; Conservative 19; Mismatches 69; Indels 52; Gaps 7;

```

QY      33 VYWN SANKRFQAE-----GGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVGGA 87
      |||| :| |||          ||| :  || ||: ||  || :  || ||:| |
Db      35 VYWN RSNPRFQVSAVG DGGGYTVEVSINDYLDIYCPHYGAPLP-PAERMERYILYMNGE 93

QY      88 QGRRCEAPPAPNLLLTCDRPDL---DLRFTIKFQEYSPNLWGHEFRSHHDYIIATSDGT 144
      |:          |:| |          |:| : ||| :|  | ||| |:| | |: :
Db      94 GHASCDHRQRGFKRWE CNRPAAPGGPLKFSEKFQLFTPFSLGFEFRPGHEYYYISATP-- 151

QY     145 REGLES LQGGVCLTRGMKVLLRVGQSPRGGA VPRKPVSEMPMERDRGAAHSLEPGKENLP 204
      :|      ||      :|| :|
Db     152 ----PNLVDRPCLR--LKVYVR-----PTNETLY 174

QY     205 GDP----TSNATSRGAEG 218
      |      |||: :  | |
Db     175 EAPEPIFTSNSSCSGLGG 192

```

RESULT 9

JE0322

QY	65	ARPPGHSSPNYEFYKLYLVG-----GAQGRCEAPPAPNLLLTCDRPDLDLR	112
Db	65	YEDSVPEDKT--ERYVLYMVNFDGYSSCDHISKGFKRWECNRPHSPN-----GPLK	113
QY	113	FTIKFQEYSPNLWGHEFRSHHDYIIATS---DGTREGLESLQGGVCLTRGMKVLLRVGQ	169
Db	114	FSEKFQLFTPFSLGFEFRPGREYFYISSAIPDNGRRS-----CLK--LKVFVR---	159
QY	170	SPRGGAVPRKPVSEMPMERDRGAAHSLEPGKENLPGDPTSNAATSRGAEGPLPPPSMP--A	227
Db	160	-PANSCMKTIGVHDRVFDVNDKVENSLPADDTV---RESAEP SRG-ENAAQTPRIPIRL	214
QY	228	VAGAAGGLALLLL	240
Db	215	LATLLELLIAMI	227

Query Match 9.2%; Score 169.5; DB 2; Length 201;
Best Local Similarity 29.9%; Pred. No. 5.4e-05;
Matches 66; Conservative 18; Mismatches 82; Indels 55; Gaps 10;

QY	24	LVSGLSL-EPVYWNSANKRFQAEGGYVLAPQIGDRDLLCPRARPPGPHSSPNYEYFKLY	82
		: : : :	
Db	20	LRGGSSLRHVVWYWNSSNPRL-LRGDAVVELGLNDYLDIVCPHYEGPGPPEGP--ETFALY	76
QY	83	LVGGAQGRRCEAP-PAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHHDYYYIIATS	141
		: : : : : :	
Db	77	MVDWPGYESCQAEGPRAYKRWVCSLPFGHVQFSEKIQRFTPFSLGFEFLPGETYYYYISVP	136
QY	142	DGTREGLES LQGGVCLTRGMKVLLRVGQSPRGAVPRKPVSEMPMERDRGAAHSLEPGKE	201
		: :	
Db	137	--TPE-----SSGQCL-----RLQVSVCCKERKSES AHPV-----	164

QY 202 NLPGDPTSNATS--RGAEGPLPPPSMPAVAGAAGGLALLLL 240
 | | : | | | | : | | | | | | |
 Db 165 ---GSPGESGTSGWRGGDTPSP-----LCLLLL 189

RESULT 12

I58170

LERK-7 precursor - human

N;Alternate names: AL-1

C;Species: Homo sapiens (man)

C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 29-Sep-1999

C;Accession: I58170; G01812

R;Winslow, J.W.; Moran, P.; Valverde, J.; Shih, A.; Yuan, J.Q.; Wong, S.C.;
 Tsai, S.P.; Goddard, A.; Henzel, W.J.; Hefti, F.
 Neuron 14, 973-981, 1995

A;Title: Cloning of AL-1, a ligand for an Eph-related tyrosine kinase receptor
 involved in axon bundle formation.

A;Reference number: I58170; MUID:95267434; PMID:7748564

A;Accession: I58170

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-228 <RES>

A;Cross-references: GB:S77167; NID:g914184; PID:g914185

R;Kozlosky, C.J.; VandenBos, T.; Park, L.S.; Cerretti, D.P.; Carpenter, M.K.
 submitted to the EMBL Data Library, May 1995

A;Reference number: G08477

A;Accession: G01812

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-228 <KOZ>

A;Cross-references: EMBL:U26403; NID:g1019430; PIDN:AAB60377.1; PID:g1019431

C;Genetics:

A;Gene: GDB:EPLG7; AF1; LERK7

A;Cross-references: GDB:568757; OMIM:601535

A;Map position: 13q33-13q33

C;Superfamily: axon guidance signal protein

Query Match 9.1%; Score 167.5; DB 2; Length 228;

Best Local Similarity 28.8%; Pred. No. 8.5e-05;

Matches 65; Conservative 29; Mismatches 81; Indels 51; Gaps 11;

QY 33 VYWNSANKRFQAEAGGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVG----- 85
 | | | | : | | | | : | | | | | | | | | |

Db 34 VYWNSSNPRFQ-RGDYHIDVCINDYLDVFCPHYEDSVPEDKT--ERYVLYMVNFDGYSAC 90

QY 86 -----GAQGRRCEAPPAPNLLLTCDRPDLRLFTIKFQEYSPNLWGHEFRSHHDAIYIIAT 140
 | : | | : | | | | : | | | | : | | |

Db 91 DHTSKGFKRWEENRPHSPN-----GPLKFSEKFQLFTPFSLGFEPFRGREYFYISS 141

QY 141 S---DGTREGLES LQGGVCLTRGMKVLLRVGQSPRGAVPRKPVSEMPMERDRGAAHSLE 197
 : : | | | | : | | : | | | : | | : | |

Db 142 AIPDNGRRS-----CLK--LKVFVR----PTNSCMKTIGVHDRVFDVNDKVENSLE 186

QY 198 PGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVA 243
 | : : | | | | : | | | | : | | |

Db 187 PADDTV---HESAEPSRG-ENAAQTPRIPSRL-----LAILLFLLA 223

A36377

Query Match 9.0%; Score 166; DB 2; Length 205;
Best Local Similarity 27.5%; Pred. No. 9.7e-05;
Matches 46; Conservative 31; Mismatches 74; Indels 16; Gaps 5;

```

QY      18 LLGVLGLVSGLSLEPVYWSANKRFQAEGGVLYPQIGDRLDLLCPRARPPGPHSSPN-- 75
      |||:  ::  |::|:|:|:|  |::|:|:|:|  ||  :
Db      8  LLGLCCSLAAADRHTVFWNSSNPKFRNE-DYTIHVQLNDYVDIICPHYE---DHSVADAA 63

QY      76 YEFYKLYLVGGAQGRRCEAPPAPNLLTCDRDPDL---DLRFTIKFQEYSPNLWGHEFRSH 132
      | | |||  : : |:  :  |::|  : : ||| : : |  | ||:
Db      64 MEQYILYLVEHEEYQLCQPQSKDQVRWQCNRPSAKHGPEKLSEKFQRFPTFTLGKEFKEG 123

QY      133 HDYIIATSDGTREGLESLOGGVCLTRGMKVLLRVGQSPRGGA VPRK 179
      | || |:  |  ||  : |  ::  ||:  |:
Db      124 HSYYYISKPIHQHEDR-----CLRLKVTVSGKITHSPQAHVNPQE 163

```

S31216

collagen alpha 1(X) chain precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Aug-1999
C;Accession: S31216; S28807; S22215; S30127; I48299; S26397; S31830
R;Kong, R.Y.C.; Kwan, K.M.; Lau, E.T.; Thomas, J.T.; Boot-Handford, R.P.; Grant,
M.E.; Cheah, K.S.E.
Eur. J. Biochem. 213, 99-111, 1993
A;Title: Intron-exon structure, alternative use of promoter and expression of
the mouse collagen X gene, Col10a-1.
A;Reference number: S31216; MUID:93238750; PMID:8477738
A;Accession: S31216
A;Molecule type: DNA
A;Residues: 1-680 <KON>
A;Cross-references: EMBL:Z21610; NID:g49793; PIDN:CAA79736.1; PID:g49794
R;Elima, K.; Eerola, I.; Rosati, R.; Metsaeranta, M.; Garofalo, S.; Peraelae,
M.; de Crombrughe, B.; Vuorio, E.
Biochem. J. 289, 247-253, 1993

A;Title: The mouse collagen X gene: complete nucleotide sequence, exon structure and expression pattern.
 A;Reference number: S28807; MUID:93143676; PMID:8424763
 A;Accession: S28807
 A;Molecule type: DNA
 A;Residues: 1-285,'A',287-680 <ELI>
 A;Cross-references: EMBL:X67348; NID:g50480; PIDN:CAA47763.1; PID:g50481
 R;Elima, K.; Metsaeranta, M.; Kallio, J.; Peraelae, M.; Eerola, I.; Garofalo, S.; de Crombrughe, B.; Vuorio, E.
 Biochim. Biophys. Acta 1130, 78-80, 1992
 A;Title: Specific hybridization probes for mouse alpha-2(IX) and alpha-1(X) collagen mRNAs.
 A;Reference number: S22215; MUID:92182017; PMID:1543751
 A;Accession: S22215
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 385-450,'K',452-627 <ELA>
 A;Cross-references: EMBL:X63013; NID:g49795; PIDN:CAA44741.1; PID:g49796
 R;Apte, S.S.; Olsen, B.R.
 Matrix 13, 165-179, 1993
 A;Title: Characterization of the mouse type X collagen gene.
 A;Reference number: S30127; MUID:93261348; PMID:8492743
 A;Accession: S30127
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-12,'F',14-26,'S',28-247,'L',249-285,'A',287-305,'F',307-416,'S',418-499,'L',501-566,'C',568,'H',570,'IY',573-634,'T',636-680 <APT>
 R;Apte, S.S.; Seldin, M.F.; Hayashi, M.; Olsen, B.R.
 Eur. J. Biochem. 206, 217-224, 1992
 A;Title: Cloning of the human and mouse type X collagen genes and mapping of the mouse type X collagen gene to chromosome 10.
 A;Reference number: I48299; MUID:92267014; PMID:1587271
 A;Accession: I48299
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 52-247,'L',249-285,'A',287-305,'F',307-416,'S',418-499,'L',501-566,'C',568,'H',570,'IY',573-634,'T',636-680 <RES>
 A;Cross-references: EMBL:X65121; NID:g50482; PIDN:CAA46237.1; PID:g667031
 R;Summers, T.A.; Irwin, M.H.; Mayne, R.; Balian, G.
 J. Biol. Chem. 263, 581-587, 1988
 A;Title: Monoclonal antibodies to type X collagen. Biosynthetic studies using an antibody to the amino-terminal domain.
 A;Reference number: S26397; MUID:88087150; PMID:2826450
 A;Accession: S26397
 A;Molecule type: protein
 A;Residues: 'SDGYFSQ',24-26,'KQ' <SUM>
 C;Genetics:
 A;Gene: Col10a-1
 A;Map position: 10
 A;Introns: 51/3
 C;Superfamily: collagen alpha 1(VIII) chain; complement Clq carboxyl-terminal homology
 C;Keywords: coiled coil; extracellular matrix; glycoprotein; homotrimer
 F;1-18/Domain: signal sequence #status predicted <SIG>
 F;19-680/Product: collagen alpha 1(X) chain #status predicted <MAT>
 F;553-679/Domain: complement Clq carboxyl-terminal homology <ClQ>

Query Match 8.6%; Score 159; DB 2; Length 680;
 Best Local Similarity 25.5%; Pred. No. 0.0011;
 Matches 97; Conservative 30; Mismatches 108; Indels 146; Gaps 24;

```

Qy      1 MGPPHSGPGGV-RVGALLLLGLVGLVSLSPVYWNSANKRFQAEAGGYVLYPQIGDRLD 59
      :||| || || | | | | | | :
Db      211 IGPP--GPSGVGRRGENGFPGQPGI-----KGDRGFPGEMG----- 244

Qy      60 LLCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCAPPAPNLLLTCDRDLRLRFTIKFQE 119
      : |||| | | | | | | | | : : : :
Db      245 ----PSGPPGPQGP-----GKQGR--EGIGKPGAIGSPGQPGI----- 277

Qy      120 YSPNLWGHEFRSHHDYIIATSDGT----REGLESQGGVCLTRGMKVLLRVGQSPRGGA 175
      | || | | | | | | | :|| | : | | | |
Db      278 --PGEKGHPGSPG-----IAGPPGAPGFGKQGLPGLRG----QRG-----PAG-- 314

Qy      176 VPRKPVSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGL 235
      : | | : : || | | | | | : | : | | | : || | :
Db      315 LPGAPGA----KGERGPAG--HPGEPGLPGSP----GNMGPQGPKGIPGNHGIPGAKGEI 364

Qy      236 ALLLLGVAGAGGAMCWRRRRAKP---SESRHPG-----PGSFGRGGSGLGLGGGGG 282
      | : | || || | | | | : : || | | : | | : || |
Db      365 G--LVGPAGPPGA---RGARGPPGLDGKTGYPGEPGLNGPKGNPGLPGQKGDPGVGGTTPG 419

Qy      283 M-----GPREAEPGELGIALRGGAADPPFCPHYEKVSGDYGHPVY 323
      : | | | | | | | | | | | | : | | : | | :
Db      420 LRGPVGPVGAKGVPGHNGEAGPR-GEPIPGTR----GPTGPPGVPGFPGSKGDPGNP-- 472

Qy      324 IVQDGP-----PQSPP 334
      || | |
Db      473 -GAPGPAGIATKGLNGPTGPP 492
  
```

RESULT 15

CGBO7S

collagen alpha 1(III) chain - bovine

C;Species: Bos primigenius taurus (cattle)

C;Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 07-May-1999

C;Accession: A02862; A38001; A38002; A38003; A38004; A38005; S71946

R;Fietzek, P.P.; Allmann, H.; Rauterberg, J.; Henkel, W.; Wachter, E.; Kuehn, K. Hoppe-Seyler's Z. Physiol. Chem. 360, 809-820, 1979

A;Title: The covalent structure of calf skin type III collagen. I. The amino acid sequence of the amino terminal region of the alpha1(III) chain (position 1-222).

A;Reference number: A02862; MUID:80026026; PMID:488906

A;Accession: A02862

A;Molecule type: protein

A;Residues: 1-242 <FIE>

R;Dewes, H.; Fietzek, P.P.; Kuehn, K.

Hoppe-Seyler's Z. Physiol. Chem. 360, 821-832, 1979

A;Title: The covalent structure of calf skin type III collagen. II. The amino acid sequence of the cyanogen bromide peptide alpha1(III)CB1,8,10,2 (positions 223-402).

A;Reference number: A38001; MUID:80026027; PMID:488907

A;Accession: A38001

A;Molecule type: protein

A;Residues: 243-422 <DEW1>

R;Bentz, H.; Fietzek, P.P.; Kuehn, K.
 Hoppe-Seyler's Z. Physiol. Chem. 360, 833-840, 1979
 A;Title: The covalent structure of calf skin type III collagen. III. The amino acid sequence of the cyanogen bromide peptide alphas(III)CB4 (positions 403-551).
 A;Reference number: A38002; MUID:80026028; PMID:488908
 A;Accession: A38002
 A;Molecule type: protein
 A;Residues: 423-571 <BEN>
 R;Lang, H.; Glanville, R.W.; Fietzek, P.P.; Kuehn, K.
 Hoppe-Seyler's Z. Physiol. Chem. 360, 841-850, 1979
 A;Title: The covalent structure of calf skin type III collagen. IV. The amino acid sequence of the cyanogen bromide peptide alphas(III)CB5 (positions 552-788).
 A;Reference number: A38003; MUID:80026029; PMID:488909
 A;Accession: A38003
 A;Molecule type: protein
 A;Residues: 572-808 <LAN>
 R;Dewes, H.; Fietzek, P.P.; Kuehn, K.
 Hoppe-Seyler's Z. Physiol. Chem. 360, 851-860, 1979
 A;Title: The covalent structure of calf skin type III collagen. V. The amino acid sequence of the cyanogen bromide peptide alphas(III)CB9A (position 789 to 927).
 A;Reference number: A38004; MUID:80026030; PMID:488910
 A;Accession: A38004
 A;Molecule type: protein
 A;Residues: 809-947 <DEW2>
 R;Allmann, H.; Fietzek, P.P.; Glanville, R.W.; Kuehn, K.
 Hoppe-Seyler's Z. Physiol. Chem. 360, 861-868, 1979
 A;Title: The covalent structure of calf skin type III collagen. VI. The amino acid sequence of the carboxyterminal cyanogen bromide peptide alphas(III)CB9B (position 928-1028).
 A;Reference number: A38005; MUID:80026031; PMID:488911
 A;Accession: A38005
 A;Molecule type: protein
 A;Residues: 948-1049 <ALL>
 A;Experimental source: skin
 R;Henkel, W.
 Biochem. J. 318, 497-503, 1996
 A;Title: Cross-link analysis of the C-telopeptide domain from type III collagen.
 A;Reference number: S71946; MUID:96404897; PMID:8809038
 A;Accession: S71946
 A;Molecule type: protein
 A;Residues: 87-106;1017-1029;1037-1049 <HEN>
 C;Comment: Prolines at the third position of the tripeptide repeating unit (G-X-Y) are hydroxylated in some or all of the chains.
 C;Comment: The type III collagen molecule is a trimer of identical chains, linked to each other by interchain disulfide bonds. Trimers are also cross-linked by allysines forming desmosine.
 C;Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology; von Willebrand factor type C repeat homology
 C;Keywords: coiled coil; extracellular matrix; glycoprotein; hydroxylysine; hydroxyproline; skin; trimer; triple helix
 F;1-1049/Product: collagen alpha 1(III) chain #status experimental <CAB>
 F;1-14/Region: amino-terminal nonhelical telopeptide
 F;15-1040/Region: helical
 F;587-589/Region: cell attachment (R-G-D) motif

F;752-754/Region: cell attachment (R-G-D) motif
 F;875-877/Region: cell attachment (R-G-D) motif
 F;878-880/Region: cell attachment (R-G-D) motif
 F;935-937/Region: cell attachment (R-G-D) motif
 F;1041-1049/Region: carboxyl-terminal nonhelical telopeptide
 F;95,107,119,938,950/Modified site: 5-hydroxylysine (Lys) #status experimental
 F;107,950/Modified site: allysine (Lys) #status predicted
 F;107/Binding site: carbohydrate (Lys) (covalent) #status experimental
 F;1040,1041/Disulfide bonds: interchain #status predicted

Query Match 8.4%; Score 154.5; DB 1; Length 1049;
 Best Local Similarity 26.5%; Pred. No. 0.0036;
 Matches 60; Conservative 9; Mismatches 74; Indels 83; Gaps 8;

```

QY      171 PRGGAVPRKPVSEMPMERDRGA-----AHSLEPGKEN 202
      | ||: | |      :::||:
Db      688 PAGGSGPAGPPGPQGVKGERGSPGGPGAAGFPGGRGPPGPPGSNGNPGPPGSSGAPGKDG 747

QY      203 LPGDPTSNAT-----SRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGA 245
      || | ||      ||| || | | | | | | | | |
Db      748 PPGPPGSNGAPGSPGISGPKGDSGPPGERGAPGPQPPGAPGPLGIAG-----LTGARGL 802

QY      246 GGAMCWRRRRRAKP-----SESRHGP-----GSFGRGSSLGLGGGGMGPREAEPGE 292
      |      | |      | : |||      | | | | | | | | : ||
Db      803 AGPPGMPGARGSPGPQGIKGENGKPGPSGQNGERGPPGPQGLPGLAGTAGEPGRDGNPGS 862

QY      293 LGIALRGG-----GAADPPFCPHYEKVSGDYGHPVYIVQDGPP 330
      |: | |      | | |      | |||      |||
Db      863 DGLPGRDGAPGAKGDRGENGSPGAP-----GAPGHP-----GPP 896
  
```

Search completed: September 15, 2004, 12:40:10
 Job time : 23.239 secs

OM protein - protein search, using sw model

Run on: September 15, 2004, 12:39:22 ; Search time 74.4151 Seconds
(without alignments)
1465.220 Million cell updates/sec

Title: US-10-021-121-4
Perfect score: 1850
Sequence: 1 MGPPHSGPGGVRV GALLLLG.....PVYIVQDGPPQSPPNIYYKV 340

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1335176 seqs, 320689617 residues

Total number of hits satisfying chosen parameters: 1335176

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query					
No.	Score	Match	Length	DB	ID	Description

1	1850	100.0	340	13	US-10-021-121-4	Sequence 4, Appli
2	1846	99.8	340	13	US-10-138-787-3	Sequence 3, Appli
3	1844	99.7	340	15	US-10-417-924A-2	Sequence 2, Appli
4	1841	99.5	455	13	US-10-021-121-2	Sequence 2, Appli
5	1559	84.3	285	16	US-10-408-765A-2695	Sequence 2695, Ap
6	632	34.2	346	13	US-10-021-121-9	Sequence 9, Appli
7	632	34.2	346	16	US-10-356-289-2	Sequence 2, Appli
8	629.5	34.0	333	9	US-09-754-105-2	Sequence 2, Appli
9	629.5	34.0	333	9	US-09-978-339-2	Sequence 2, Appli
10	629.5	34.0	333	13	US-10-021-121-10	Sequence 10, Appl
11	629.5	34.0	333	15	US-10-331-496A-63	Sequence 63, Appl
12	622.5	33.6	333	13	US-10-138-787-4	Sequence 4, Appli
13	608.5	32.9	345	13	US-10-138-787-5	Sequence 5, Appli
14	498	26.9	89	9	US-09-862-179A-17	Sequence 17, Appl
15	498	26.9	89	13	US-10-138-787-13	Sequence 13, Appl
16	284.5	15.4	92	9	US-09-864-761-48262	Sequence 48262, A
17	205.5	11.1	136	9	US-09-864-761-48257	Sequence 48257, A
18	202.5	10.9	106	9	US-09-925-297-639	Sequence 639, App
19	201	10.9	82	9	US-09-862-179A-15	Sequence 15, Appl
20	201	10.9	82	13	US-10-138-787-11	Sequence 11, Appl
21	200.5	10.8	82	9	US-09-862-179A-16	Sequence 16, Appl
22	200.5	10.8	82	13	US-10-138-787-12	Sequence 12, Appl
23	179	9.7	238	9	US-09-904-954-2	Sequence 2, Appli
24	179	9.7	238	10	US-09-733-756-2	Sequence 2, Appli
25	179	9.7	238	14	US-10-241-220-72	Sequence 72, Appl
26	179	9.7	238	15	US-10-295-027-130	Sequence 130, App
27	176	9.5	209	9	US-09-921-984-2	Sequence 2, Appli
28	174.5	9.4	233	13	US-10-138-787-7	Sequence 7, Appli
29	172.5	9.3	218	9	US-09-925-297-510	Sequence 510, App
30	169.5	9.2	201	9	US-09-904-954-4	Sequence 4, Appli
31	169.5	9.2	225	16	US-10-322-696-135	Sequence 135, App
32	169	9.1	201	13	US-10-138-787-8	Sequence 8, Appli
33	168.5	9.1	209	13	US-10-138-787-6	Sequence 6, Appli
34	167.5	9.1	228	8	US-08-578-684-4	Sequence 4, Appli
35	166	9.0	205	13	US-10-138-787-10	Sequence 10, Appl
36	166	9.0	205	14	US-10-171-311-50	Sequence 50, Appl
37	166	9.0	205	15	US-10-372-683-34	Sequence 34, Appl
38	164.5	8.9	204	12	US-10-147-493-288	Sequence 288, App
39	164.5	8.9	204	12	US-10-145-127-288	Sequence 288, App
40	164.5	8.9	204	12	US-10-160-503-288	Sequence 288, App
41	164.5	8.9	204	12	US-10-143-118-288	Sequence 288, App
42	164.5	8.9	204	12	US-10-144-993-288	Sequence 288, App
43	164.5	8.9	204	12	US-10-158-787-288	Sequence 288, App
44	164.5	8.9	204	12	US-10-140-024-288	Sequence 288, App
45	164.5	8.9	204	12	US-10-140-308-288	Sequence 288, App

ALIGNMENTS

RESULT 1
 US-10-021-121-4
 ; Sequence 4, Application US/10021121
 ; Publication No. US20020142444A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Caras, Ingrid W

```

; TITLE OF INVENTION: A2-1 Neurotrophic Factor
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/021,121
; FILING DATE: 06-Dec-2001
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/635,130
; FILING DATE: 19-Mar-1996
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Torchia, PhD., Timothy E.
; REGISTRATION NUMBER: 36,700
; REFERENCE/DOCKET NUMBER: P1001
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
;
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 340 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-021-121-4

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Query Match          100.0%; Score 1850; DB 13; Length 340;
Best Local Similarity 100.0%; Pred. No. 6.6e-136;
Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MGPPHSGPGGVRVGALLLLGVGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MGPPHSGPGGVRVGALLLLGVGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60

Qy     61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120

Qy    121 SPNLWGHEFRSHHDYIIATSDGTREGLESQGQVCLTRGMKVLLRVGQSPRGGAVPRKP 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 SPNLWGHEFRSHHDYIIATSDGTREGLESQGQVCLTRGMKVLLRVGQSPRGGAVPRKP 180

Qy    181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240

Qy    241 GVAGAGGAMCWRRRRAKPSERHPGPGSFGRGGSGLGLGGGGMGPREAEPGELGIALRGG 300

```

```

Db      241  |||||GVAGAGGAMCWRRRRAKPSERHPGPGSFGRGGSGLGLGGGGMGMPREAEPGELGIALRGG 300
QY      301  GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYYKV 340
Db      301  |||||GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYYKV 340

```

RESULT 2

US-10-138-787-3

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; Sequence 3, Application US/10138787
; Publication No. US20020172984A1
; GENERAL INFORMATION:
; APPLICANT: Holland, Sacha
; APPLICANT: Mbamalu, Geraldine
; APPLICANT: Pawson, Tony
; TITLE OF INVENTION: OLIGOMERIZED RECEPTORS WHICH AFFECT PATHWAYS REGULATED
; TITLE OF INVENTION: BY TRANSMEMBRANE LIGANDS FOR ELK-RELATED RECEPTOR
; TITLE OF INVENTION: TYROSINE KINASES
; FILE REFERENCE: 11757.23USWO
; CURRENT APPLICATION NUMBER: US/10/138,787
; CURRENT FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: US/09/214,631
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: PCT/CA97/00473
; PRIOR FILING DATE: 1997-07-04
; PRIOR APPLICATION NUMBER: 60/021,272
; PRIOR FILING DATE: 1996-07-05
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 340
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-138-787-3

```

```

Query Match          99.8%; Score 1846; DB 13; Length 340;
Best Local Similarity 99.7%; Pred. No. 1.3e-135;
Matches 339; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

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QY      1  MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEAGGYVLYPQIGDRLDL 60
Db      1  |||||MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEAGGYVLYPQIGDRLDL 60
QY     61  LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120
Db     61  |||||LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120
QY    121  SPNLWGHEFRSHHDYIIATSDGTREGLESQGQVCLTRGMKVLLRVGQSPRGGA VPRKP 180
Db    121  |||||SPNLWGHEFRSHHDYIIATSDGTREGLESQGQVCLTRGMKVLLRVGQSPRGGA VPRKP 180
QY    181  VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240
Db    181  |||||VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240
QY    241  GVAGAGGAMCWRRRRAKPSERHPGPGSFGRGGSGLGLGGGGMGMPREAEPGELGIALRGG 300

```

```

Db      241  |||||
          GVAGAGGAMCWRRRRRAKPSES RHPGPGSFGRGGS LGLGGGGMGMPREAE PGELGIALRGG 300

QY      301  GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYYKV 340
          |||||
Db      301  GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYYKV 340

```

RESULT 3

```

US-10-417-924A-2
; Sequence 2, Application US/10417924A
; Publication No. US20030215918A1
; GENERAL INFORMATION:
; APPLICANT: Samuel Davis, et al.
; TITLE OF INVENTION: BIOLOGICALLY ACTIVE EPH FAMILY LIGANDS
; FILE REFERENCE: REG-341Z
; CURRENT APPLICATION NUMBER: US/10/417,924A
; CURRENT FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: 09/051,994
; PRIOR FILING DATE: 1998-04-24
; PRIOR APPLICATION NUMBER: PCT/US96/17201
; PRIOR FILING DATE: 1996-10-25
; PRIOR APPLICATION NUMBER: 60/007,015
; PRIOR FILING DATE: 1995-10-25
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 340
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: Misc. feature
; LOCATION: (166)
; OTHER INFORMATION: Xaa = unknown or other
US-10-417-924A-2

```

```

Query Match          99.7%; Score 1844; DB 15; Length 340;
Best Local Similarity 99.7%; Pred. No. 1.9e-135;
Matches 339; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY      1  MGPPHSGPGGVRV GALLLLGLVGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60
          |||||
Db      1  MGPPHSGPGGVRV GALLLLGLVGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60

QY      61  LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPLDLRFTIKFQEY 120
          |||||
Db      61  LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPLDLRFTIKFQEY 120

QY      121 SPNLWGHEFRSHHDYIIATSDGTREGLES LQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180
          |||||
Db      121 SPNLWGHEFRSHHDYIIATSDGTREGLES LQGGVCLTRGMKVLLXVGQSPRGGAVPRKP 180

QY      181 VSEMPMERDRGAAHSLEPGKENLPGDPTS NATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240
          |||||
Db      181 VSEMPMERDRGAAHSLEPGKENLPGDPTS NATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240

QY      241 GVAGAGGAMCWRRRRRAKPSES RHPGPGSFGRGGS LGLGGGGMGMPREAE PGELGIALRGG 300

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```

Db      241  |||||GVAGAGGAMCWRRRRAKPSERSHPGPGSFGRGSLGLGGGGMGMPREAEPEGELGIALRGG 300
QY      301  GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYYKV 340
Db      301  |||||GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYYKV 340

```

RESULT 4

US-10-021-121-2

; Sequence 2, Application US/10021121

; Publication No. US20020142444A1

; GENERAL INFORMATION:

; APPLICANT: Caras, Ingrid W

; TITLE OF INVENTION: A2-1 Neurotrophic Factor

; NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 1 DNA Way

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WinPatin (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/021,121

; FILING DATE: 06-Dec-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/635,130

; FILING DATE: 19-Mar-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Torchia, PhD., Timothy E.

; REGISTRATION NUMBER: 36,700

; REFERENCE/DOCKET NUMBER: P1001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650/225-8674

; TELEFAX: 650/952-9881

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 455 amino acids

; TYPE: Amino Acid

; TOPOLOGY: Linear

; SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-10-021-121-2

Query Match 99.5%; Score 1841; DB 13; Length 455;

Best Local Similarity 100.0%; Pred. No. 4.7e-135;

Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY      1  MGPPHSGPGGVRVGALLLLGVGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60
Db      1  MGPPHSGPGGVRVGALLLLGVGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60

```

QY 61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPLDLRFTIKFQEY 120
 |||
 Db 61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPLDLRFTIKFQEY 120

QY 121 SPNLWGHEFRSHHDYIIATSDGTREGLESQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180
 |||
 Db 121 SPNLWGHEFRSHHDYIIATSDGTREGLESQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180

QY 181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLL 240
 |||
 Db 181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLL 240

QY 241 GVAGAGGAMCWRRRRRAKPSESHPGPSFGRGGSGLGLGGGGMGPREAEPGELGIALRGG 300
 |||
 Db 241 GVAGAGGAMCWRRRRRAKPSESHPGPSFGRGGSGLGLGGGGMGPREAEPGELGIALRGG 300

QY 301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY 338
 |||
 Db 301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY 338

RESULT 5

US-10-408-765A-2695

; Sequence 2695, Application US/10408765A

; Publication No. US20040101874A1

; GENERAL INFORMATION:

; APPLICANT: Ghosh, Soumitra S.

; APPLICANT: Fahy, Eoin D.

; APPLICANT: Zhang, Bing

; APPLICANT: Gibson, Bradford W.

; APPLICANT: Taylor, Steven W.

; APPLICANT: Glenn, Gary M.

; APPLICANT: Warnock, Dale E.

; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION

; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME

; FILE REFERENCE: 660088.465

; CURRENT APPLICATION NUMBER: US/10/408,765A

; CURRENT FILING DATE: 2003-04-04

; NUMBER OF SEQ ID NOS: 3077

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 2695

; LENGTH: 285

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-408-765A-2695

Query Match 84.3%; Score 1559; DB 16; Length 285;

Best Local Similarity 100.0%; Pred. No. 2.5e-113;

Matches 285; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 56 DRDLLLCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPLDLRFTI 115
 |||
 Db 1 DRDLLLCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPLDLRFTI 60

QY 116 KFQEYSPNLWGHEFRSHHDYIIATSDGTREGLESQGGVCLTRGMKVLLRVGQSPRGG 175
 |||

Db 61 KFQEYSPNLWGHEFRSHHDYIIATSDGTREGLES LQGGVCLTRGMKVLLRVGQSPRGA 120
 QY 176 VPRKPVSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGL 235
 ||||||||||||||||||||||||||||||||||||||||||||
 Db 121 VPRKPVSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGL 180
 QY 236 ALLLLGVAGAGGAMCWRRRRAKPSESRHPGPGSFGRGGS LGLGGGGMGPREAEPGELGI 295
 ||||||||||||||||||||||||||||||||||||||||||||
 Db 181 ALLLLGVAGAGGAMCWRRRRAKPSESRHPGPGSFGRGGS LGLGGGGMGPREAEPGELGI 240
 QY 296 ALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYYKV 340
 ||||||||||||||||||||||||||||||||||||||||||||
 Db 241 ALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYYKV 285

RESULT 6

US-10-021-121-9

; Sequence 9, Application US/10021121

; Publication No. US20020142444A1

; GENERAL INFORMATION:

; APPLICANT: Caras, Ingrid W

; TITLE OF INVENTION: A2-1 Neurotrophic Factor

; NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 1 DNA Way

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WinPatin (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/021,121

; FILING DATE: 06-Dec-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/635,130

; FILING DATE: 19-Mar-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Torchia, PhD., Timothy E.

; REGISTRATION NUMBER: 36,700

; REFERENCE/DOCKET NUMBER: P1001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650/225-8674

; TELEFAX: 650/952-9881

; INFORMATION FOR SEQ ID NO: 9:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 346 amino acids

; TYPE: Amino Acid

; TOPOLOGY: Linear

; SEQUENCE DESCRIPTION: SEQ ID NO: 9:

US-10-021-121-9

Query Match 34.2%; Score 632; DB 13; Length 346;
 Best Local Similarity 39.5%; Pred. No. 5e-41;
 Matches 145; Conservative 48; Mismatches 116; Indels 58; Gaps 9;

```

Qy      8 PGGVRVGALLLLGVLGLVSL-----SLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLL 61
      ||  :|  |:  |:  :|  :|||  |:|  |:|  :|  |:|:|:|:|:|:|:
Db      4 PGQRWLKGWLVAMVVWALCRLATPLAKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDII 63

Qy     62 CPRARPPGPHSSPNYEFYKLYLVGGAQGRCEAPPAPNLLLTCDRPLDLRFTIKFQEYS 121
      |||  |  ||:|||||  |  |  ||:|:|:|:|:|:|:|:|:|:|:|:|:
Db     64 CPRAEAGRP-----YEEYKLYLVRPEQAAACSTVLDPNVLVTNCRPEQEIRFTIKFQEFS 118

Qy    122 PNLWGHEFRSHHDYIIATSDGTREGLESLOGGVCLTRGMKVLLRVGQSPRGGA VPRKPV 181
      ||  |  |:  |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
Db    119 PNYMGLEFKKHHDYIITSTSNGLSLEGLNREGGVCRTMTMKIIMKVGQDPNAVTPPEQLTT 178

Qy    182 SEMPMERDRGAAHSLE-PGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLA---- 236
      |  |  |  :  :  ||  ||  :  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db    179 SRPSKEADNTVKMATQAPGSRGSLGSDGKHETVNQEEKSGP-----GASGGSSGDPD 231

Qy    237 -----LLLLGVAGAGGA-----MCWRRRRRAKPSESRRHPGPGSFGRGGSLSGL 277
      :  |  ||  :  |:|  |  :  :  |  |  |  |  |  |  |  |  |  |  |  |
Db    232 GFFNSKVALFAAVGAGCVIFLLIIIFLTVLLKLKRHRKHHTQQ-----RAAALS 282

Qy    278 ----GGGGMGPREAEPGELGIALRGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP 333
      ||  |  ||  :  :  ||  :  :  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db    283 STLASPKGSGTAGTEPSDIIPLR---TTENNYCPHYEKVSGDYGHPVYIVQEMPPQSP 339

Qy    334 PNIYYKV 340
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Db    340 ANIYYKV 346
  
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RESULT 7

US-10-356-289-2

; Sequence 2, Application US/10356289

; Publication No. US20040022767A1

GENERAL INFORMATION:

; APPLICANT: Lyman, Stewart D.

; APPLICANT: Beckmann, M. Patricia

; APPLICANT: Baum, Peter R.

; APPLICANT: Carpenter, Melissa K.

; TITLE OF INVENTION: NOVEL CYTOKINE DESIGNATED ELK LIGAND

; FILE REFERENCE: GENENT.67CPDV3

; CURRENT APPLICATION NUMBER: US/10/356,289

; CURRENT FILING DATE: 2003-01-31

; PRIOR APPLICATION NUMBER: US/09/039,642B

; PRIOR FILING DATE: 1998-03-16

; PRIOR APPLICATION NUMBER: 08/213,403

; PRIOR FILING DATE: 1994-03-15

; PRIOR APPLICATION NUMBER: 07/977,693

; PRIOR FILING DATE: 1992-11-13

; PRIOR APPLICATION NUMBER: 08/747,240

; PRIOR FILING DATE: 1996-10-12

; PRIOR APPLICATION NUMBER: 08/460,741

; PRIOR FILING DATE: 1995-06-02

; NUMBER OF SEQ ID NOS: 5

; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 346
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-356-289-2

Query Match 34.2%; Score 632; DB 16; Length 346;
Best Local Similarity 39.5%; Pred. No. 5e-41;
Matches 145; Conservative 48; Mismatches 116; Indels 58; Gaps 9;

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QY      8 PGGVRVGALLLLGVLGLVSGL-----SLEPVYWNSANKRFQAEAGGYVLYPQIGDRLDLL 61
      ||  :| |: |: : |      :||| |:| |:| : | |:|:|:|:|:|:|
Db      4 PGQRWLKGWLVMVWALCRLATPLAKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDII 63

QY     62 CPRARPPGPHSSPNYEFYKLYLVGGAQGRRC EAPPAPNLLLTCDRPDLRLFTIKFQEYS 121
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     64 CPRAEAGRP-----Y EYYKLYLVRPEQAAACSTVLDPNVLVTCNRPEQEIRFTIKFQEFS 118

QY    122 PNLWGHEFRSHHDYIIATSDGTREGLES LQGGVCLTRGMKVLLRVGQSPRGGAVPRKPV 181
      || | | |: | | | | | | | | | | | | | | | | | | | | | |
Db    119 PNYMGLEFKKHHDYITSTSNGLSLEGLNREGGVCRTRTMKIIMKVGQDPNAVTP EQLT 178

QY    182 SEMP MERDRGAAHSLE-PGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLA---- 236
      | | | | : : || | | | | : | | | | | | | | | | | | |
Db    179 SRPSKEADNTVKMATQAPGSRGSLGSDSGKHETV NQEEKSGP-----GASGGSSGDPD 231

QY    237 -----LLLLGVAGAGGA-----MCWRRRRRAKPSES RHPGPGSFGRGGS LGL 277
      : | | | | | | | | | | | | | | | | | | | | | | | |
Db    232 GFFNSKVALFAAVGAGCVIFLLIIIFLTVLLLKLRKRHRKHTQQ-----RAAALS L 282

QY    278 ----GGGGGMGPRAEAPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP 333
      || | | | | : : | | | | : : | | | | | | | | | | | | |
Db    283 STLASPKGSGTAGTEPSDIIIPLR---TTENNYCPHYEKVSGDYGHPVYIVQEMP PQSP 339

QY    334 PNIYYKV 340
      |||||
Db    340 ANIYYKV 346
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RESULT 8

US-09-754-105-2

; Sequence 2, Application US/09754105
; Patent No. US20010009768A1
; GENERAL INFORMATION:
; APPLICANT: Cerretti, Douglas
; APPLICANT: Reddy, Pranhitha
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING CYTOKINE DESIGNATED LERK-5
; FILE REFERENCE: 28232
; CURRENT APPLICATION NUMBER: US/09/754,105
; CURRENT FILING DATE: 2001-01-03
; PRIOR APPLICATION NUMBER: 09/329,531
; PRIOR FILING DATE: 1999-06-10
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 333

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; TYPE: PRT
; ORGANISM: homo sapiens
US-09-754-105-2
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Query Match      34.0%; Score 629.5; DB 9; Length 333;  
Best Local Similarity 40.9%; Pred. No. 7.4e-41;  
Matches 135; Conservative 52; Mismatches 130; Indels 13; Gaps 5;
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Qy 14 GALLLLGLVGLVSGLSLEPVYWN SANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSS 73
| : :: | : : ||| : ||| : | : | | | | | | : : : : : :

Db 14 GVLMVLCRTAISKSIVLEPIYWNS SN SKFLPGQGVLVLPQIGDKLDIICPKV---DSKTV 70

Qy 74 PNYEFYKLYLVGGAQGRRC EAPPAPNLLLTCDRPDL DL RFTIKFQEYSPNLWGHEFRSHH 133
|| : || : : | | | | | : || | : || | : || | | | | : || : :

Db 71 QQYEYYKVYMVDKDQADRCTIK KENTPLLNCAKPDQDIKF TIKFQEFSPNLWGLEFQKNK 130

Qy 134 DYYIIATSDGTREGLES LQGGVC LTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR 190
|||| : || : : ||| : : ||| || | : || : || | | | : | : | :

Db 131 DYYIIISTNGSLEGLDNQEGGVCQ TRAMKIIMKVGDASSAGSTRNKDPTRRPELEAGTN 190

Qy 191 GAAHSLEPGKENLPGDPTS NATSRGAEGPLPPPSMPA VAGAAGGLALLLLGVAGAGGAMC 250
| : : | : || | : : : : : : || | | : : : : :

Db 191 GRSSTTSPFVKPNPGSSTDG NSAGHSGNNILGSEVALFAGIASGC IIFVIIITLVLLLL 250

Qy 251 WRRRRRAKPSES RH PGGS FGRGGS LG LGGGGMGPREAE PGELGIALRGGAADPPFC PH 310
||| : : | | : | : | : || : : | || | | |||

Db 251 KYRRRH RKHS PQHTTTLSLSTLAT PKRSGNN----NGSEP SDIIIPLR---TADSVFC PH 303

Qy 311 YEKVSGDYGHVPVIYVQDGPPQS PPNIYYKV 340
||||| ||| ||| ||| : ||| ||| ||| |||

Db 304 YEKVSGDYGHVPVIYVQEMPPQ SPANIYYKV 333

RESULT 9

US-09-978-339-2

; Sequence 2, Application US/09978339

; Patent No. US20020103358A1

; GENERAL INFORMATION:

APPLICANT: Cerretti, Douglas P.

Reddy, Pranhitha

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; NUMBER OF SEQUENCES: 3
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CORRESPONDENCE ADDRESS:

ADDRESSEE: Immunex Corporation

STREET: 51 University Street

; CITY: Seattle

; STATE: Washington

; COUNTRY: US

; ZIP: 98101

; COMPUTER READABLE FORM:

```

; MEDIUM TYPE: Floppy disk

```

```

; COMPUTER: Apple Macintosh

```

```

;               OPERATING SYSTEM: Apple 7.1

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SOFTWARE: Microsoft Word, Version 5.1a

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; CURRENT APPLICATION DATA:

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APPLICATION NUMBER: US/09/978.339

FILING DATE: 15-Oct-2001

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; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/271,948
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2823
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 333 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-978-339-2

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Query Match          34.0%; Score 629.5; DB 9; Length 333;
Best Local Similarity 40.9%; Pred. No. 7.4e-41;
Matches 135; Conservative 52; Mismatches 130; Indels 13; Gaps 5;

```

```

Qy      14 GALLLLGLVGLVSGLSLEPVYWNSANKRFQAEAGGYVLYPQIGDRLDLLCPRARPPGPHSS 73
      | |::| : : ||:||||:| :| | |||||:|::|: :
Db      14 GVLMVLCRTAISKIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV 70

Qy      74 PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRDLRLFTIKFQEYSPNLWGHEFRSHH 133
      ||:|:|:| | | | | :|| |::| |||||:| ||| | :| :
Db      71 GQY EYKVMVDKQADRCTIKKENTPLLNCAKPDQDIKFTIKFQEFSPNLWGLEFQKNK 130

Qy     134 DYYIIATSDGTREGLES LQGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR 190
      ||||:|:|:| |||:: :||| | | ||:|:| | | : | :|
Db     131 DYYIISTSNGLSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSTRNKDPTRRPELEAGTN 190

Qy     191 GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC 250
      | : : | : | | : : : : : : | | | : : : :
Db     191 GRSSTTSPFVKPNPGSSTDGNSAGHSGNNILGSEVALFAGIASGCIIFIVIIITLVVLLL 250

Qy     251 WRRRRRAKPSES RHPGPGSFGRGGS LGLGGGGMGPREAEPGELGIALRGGGAADPPFCPH 310
      ||| : :| | : : | : || : : | | | || |||
Db     251 KYRRRRHRKHSPQHTTTLSLSTLATPKRSGNN---NGSEPSDIIIPLR---TADSVFCPH 303

Qy     311 YEKVSGDYGHPVYIVQDGPPQSPPNIYYKV 340
      ||||| |||||: |||| |||||
Db     304 YEKVSGDYGHPVYIVQEMPPQSPANIYYKV 333

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RESULT 10

US-10-021-121-10

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; Sequence 10, Application US/10021121
; Publication No. US20020142444A1
; GENERAL INFORMATION:
; APPLICANT: Caras, Ingrid W
; TITLE OF INVENTION: A2-1 Neurotrophic Factor

```

```

; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Genentech, Inc.
;   STREET: 1 DNA Way
;   CITY: South San Francisco
;   STATE: California
;   COUNTRY: USA
;   ZIP: 94080
;
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: WinPatin (Genentech)
;
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/10/021,121
;   FILING DATE: 06-Dec-2001
;   CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/08/635,130
;   FILING DATE: 19-Mar-1996
;
; ATTORNEY/AGENT INFORMATION:
;   NAME: Torchia, PhD., Timothy E.
;   REGISTRATION NUMBER: 36,700
;   REFERENCE/DOCKET NUMBER: P1001
;
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 650/225-8674
;   TELEFAX: 650/952-9881
;
; INFORMATION FOR SEQ ID NO: 10:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 333 amino acids
;     TYPE: Amino Acid
;     TOPOLOGY: Linear
;
;   SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-021-121-10

```

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Query Match          34.0%; Score 629.5; DB 13; Length 333;
Best Local Similarity 40.9%; Pred. No. 7.4e-41;
Matches 135; Conservative 52; Mismatches 130; Indels 13; Gaps 5;

```

```

Qy      14 GALLLLGVLGLVSGLSLEPVYWNNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSS 73
      | |::| : : |||:||||:| :| | |||||:|::|: :
Db      14 GVLMLVCRTAISKSIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV 70

Qy      74 PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLRLFTIKFQEYSPNLWGHEFRSHH 133
      ||::|:|:| | || || | :|| :|||:||||:||||| ||: :
Db      71 GQYEYYKVYMVVDKDQADRCTIKKENTPLLNCAKFDQDIKFTIKFQEFSPNLWGLEFQKNK 130

Qy     134 DYYIIATSDGTREGLESQGVCCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR 190
      ||||:|:|:| ||:: :||| || ||:|:| || | : | :|
Db     131 DYYIISTSNGLSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSTRNKDPTRPELEAGTN 190

Qy     191 GAAHSLEPGKENLPGDPTSNAISRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC 250
      | : : | : || | : : : : : || | | : : : :
Db     191 GRSSTTSPFVKPNPGSSSTDGNSAGHSGNNILGSEVALFAGIASGCIIFIVIIITLVVLL 250

Qy     251 WRRRRRAKPSESRRHPGPGSFGRGGSGLGGGGGMGPRAEPGELGIALRGGAADPPFCPH 310
      ||| : :| | : | :|| : : | || |||

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```

Db      14 GVLMLVLCRTAISKSIVLEPIYWNSSNSKFLPGQGGLVLYPQIGDKLDIICPKV---DSKTV 70
QY      74 PNYEFYKLYLVGGAQGRRC EAPPAPNLLLTCDRPLDLRFTTIKFQEYSPNLWGHEFRSHH 133
      ||::||::|| | || | | :|| |::||| |||::||| | | :
Db      71 GQY EYYKVYMV DDKDQADRCTIKKENTPLL NCAKPDQDIKFTIKFQEFSPNLWGLEFQKNK 130
QY      134 DYYIIATSDGTREGLES LQGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR 190
      |||::||::|| | |:: : ||| | | |::|::|| | | : | : |
Db      131 DYYIIISTSNGLSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSTRNKDPTRRPELEAGTN 190
QY      191 GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC 250
      | : : | : || | : : : : : | | | | : : : : :
Db      191 GRSSTTSPFVKPNPGSSTDGNSAGHSNNILGSEVALFAGIASGCIIFIVIIITLVVLLL 250
QY      251 WRRRRRAKPSES RHPGPGSFGRGGS LGLGGGGMGPREAEPGELGIALRGGGAADPPFCPH 310
      ||| : : | | : | : | : | : | | | | |
Db      251 KYRRRRHRKHSPQH TTTLSLSTLATPKRSGNN---NGSEPSDIIPLR---TADSVFCPH 303
QY      311 YEKVSGDYGHPVYIVQDGPPQSPPNIIYKV 340
      ||| ||| ||| ||| ||| : ||| ||| ||| ||| |||
Db      304 YEKVSGDYGHPVYIVOEMPPQSPANIYKV 333

```


Search completed: September 15, 2004, 12:55:54
Job time : 75.4151 secs

OM protein - protein search, using sw model

Run on: September 15, 2004, 12:29:25 ; Search time 65.8616 Seconds
(without alignments)
1628.811 Million cell updates/sec

Title: US-10-021-121-4
Perfect score: 1850
Sequence: 1 MGPPHSGPGGVRVGALLLLG.....PVYIVQDGPPQSPPNIYYKV 340

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertibrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

8

Result	Query				
No.	Score	Match	Length	ID	Description

1	923	49.9	331	13	Q90Z31	Q90z31 brachydanio
2	919	49.7	327	13	Q9PT69	Q9pt69 xenopus lae
3	629.5	34.0	333	13	Q9PUJ4	Q9puj4 gallus gall
4	616	33.3	341	13	Q90Z33	Q90z33 brachydanio
5	605.5	32.7	334	13	Q90Z32	Q90z32 brachydanio
6	340	18.4	205	13	Q9W6H9	Q9w6h9 xenopus lae
7	214.5	11.6	237	5	Q9U3M2	Q9u3m2 caenorhabdi
8	198.5	10.7	279	5	Q9U474	Q9u474 caenorhabdi
9	182	9.8	652	5	Q9V4E1	Q9v4e1 drosophila
10	178.5	9.6	202	13	Q98TZ1	Q98tz1 gallus gall
11	168.5	9.1	205	4	Q8N578	Q8n578 homo sapien
12	167	9.0	205	11	Q9D7K8	Q9d7k8 mus musculu
13	163.5	8.8	206	11	Q9CZS8	Q9czs8 mus musculu
14	156	8.4	675	6	Q9N178	Q9n178 sus scrofa
15	155	8.4	229	13	Q93431	Q93431 brachydanio
16	153.5	8.3	217	13	Q7SY61	Q7sy61 xenopus lae
17	153.5	8.3	1691	11	Q9ESQ2	Q9esq2 mus musculu
18	151.5	8.2	1447	13	Q9IB91	Q9ib91 xenopus lae
19	149	8.1	325	5	O17036	O17036 caenorhabdi
20	149	8.1	569	5	Q17208	Q17208 bombyx mori
21	148.5	8.0	316	5	Q19111	Q19111 caenorhabdi
22	147	7.9	921	11	Q8BSQ4	Q8bsq4 mus musculu
23	147	7.9	2936	6	Q7YRK8	Q7yrk8 canis famil
24	146.5	7.9	888	11	Q8CCZ8	Q8ccz8 mus musculu
25	146.5	7.9	1140	11	Q61434	Q61434 mus musculu
26	146.5	7.9	1449	13	Q802B5	Q802b5 xenopus lae
27	146.5	7.9	1491	13	Q91718	Q91718 xenopus lae
28	146.5	7.9	1491	13	Q7ZTM4	Q7ztm4 xenopus lae
29	146	7.9	675	13	Q90800	Q90800 gallus gall
30	146	7.9	1669	11	Q9QZS0	Q9qzs0 mus musculu
31	145.5	7.9	305	5	O17805	O17805 caenorhabdi
32	145.5	7.9	308	5	Q94620	Q94620 meloidogyne
33	145	7.8	680	11	Q9D0D2	Q9d0d2 mus musculu
34	144.5	7.8	309	5	Q25466	Q25466 meloidogyne
35	144.5	7.8	1269	13	Q7T2Z7	Q7t2z7 gallus gall
36	144.5	7.8	1347	4	Q96QB3	Q96qb3 homo sapien
37	144.5	7.8	1420	13	Q90W37	Q90w37 gallus gall
38	143.5	7.8	775	16	Q9F342	Q9f342 streptomyce
39	143	7.7	445	5	Q8MZ49	Q8mz49 drosophila
40	143	7.7	1684	6	Q8HYC1	Q8hyc1 canis famil
41	143	7.7	1688	6	Q866Z2	Q866z2 canis famil
42	143	7.7	1747	5	Q26640	Q26640 strongyloce
43	142	7.7	1034	11	Q8K229	Q8k229 mus musculu
44	142	7.7	1497	11	Q7TMS0	Q7tms0 mus musculu
45	142	7.7	1835	13	Q9IAU4	Q9iau4 gallus gall

ALIGNMENTS

RESULT 1

Q90Z31

ID Q90Z31 PRELIMINARY; PRT; 331 AA.

AC Q90Z31;

DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Ephrin B3.
 GN EFNB3.
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21290827; PubMed=11397014;
 RA Chan J., Mably J.D., Serluca F.C., Chen J.N., Goldstein N.B.,
 RA Thomas M.C., Cleary J.A., Brennan C., Fishman M.C., Roberts T.M.;
 RT "Morphogenesis of prechordal plate and notochord requires intact
 RT eph/ephrin b signaling."
 RL Dev. Biol. 234:470-482(2001).
 DR EMBL; AF375227; AAK64277.1; -.
 DR ZFIN; ZDB-GENE-010618-3; efnb3.
 DR GO; GO:0016020; C:membrane; IEA.
 DR InterPro; IPR008972; Cupredoxin.
 DR InterPro; IPR001799; Ephrin.
 DR Pfam; PF00812; Ephrin; 1.
 DR PRINTS; PR01347; EPHRIN.
 DR ProDom; PD002533; Ephrin; 1.
 DR PROSITE; PS01299; EPHRIN; 1.
 SQ SEQUENCE 331 AA; 35638 MW; 6A5EACD509A09818 CRC64;

Query Match 49.9%; Score 923; DB 13; Length 331;
 Best Local Similarity 54.8%; Pred. No. 7.9e-64;
 Matches 190; Conservative 43; Mismatches 74; Indels 40; Gaps 10;

Qy	10	GVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEAGGYVLYPQIGDRLDLLCPRARPPG	69
		: : : : : : : : : : :	
Db	9	GLGILLIFLVDLLG-ITATNMEPIYWNSLNKRFSDDKGYVLYPQIGDRLDLICPSSDPPG	67
Qy	70	PHSSPNYEFYKLYLVGG-AQGRRCCEAPPAPNLLLTCDRDLRFTIKFQEYSPNLWGHE	128
		: : : : : :	
Db	68	PRAPADYEEYKLYLVSSREQADRCEVTGAPNLLLTCDKPNSDMRFTIKFQEYSPNLWGHE	127
Qy	129	FRSHHDYIIATSDGTREGLES LQGGVCLTRGMKVLLRVGQSPRG-GAVPRKPVSEMPME	187
		: : : : : : : : :	
Db	128	FKTNHDFIIATSDGTRQGLES MRGGVCATQGMKVVLKVGQSPYGLPAKSPKPDS-----	182
Qy	188	RDRGAHSLEPGKENLPGDPTS NAT-----SRGAEGPLPPPSMPAVAGAAGGLALLL	239
		: : : : :	
Db	183	-----AGRINNPNPGTGNSTHPQIPPRGSGGENGPLPASNIAVIAGAAGGSAFLL	232
Qy	240	LGVAGAGGAMCWRRRRRAKPSESRHPGPGSFG-----RGGSLGLGGGGMGPREAEPGEL	293
		: : : : : :	
Db	233	L-VTAVICVVCYRRRHAKHSESHHP-PLSLSSLTSPKRGCGGGVGGGNNNG---SEPSDI	287
Qy	294	GIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYYKV	340
		: : :	
Db	288	IIPLR---TSDSAYCPHYEKVSGDYGHPVYIVQEMPPQSPANIYYKV	331

RESULT 2
 Q9PT69

ID Q9PT69 PRELIMINARY; PRT; 327 AA.
AC Q9PT69;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Ephrin-B3 precursor.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=20099673; PubMed=10633856;
RA Helbling P.M., Saulnier D.M.E., Robinson V., Christiansen J.H.,
RA Wilkinson D.G., Brandli A.W.;
RT "Comparative analysis of embryonic gene expression defines potential
RT interaction sites for Xenopus EphB4 receptors with ephrin-B ligands.";
RL Dev. Dyn. 216:361-373(1999).
DR EMBL; AJ236866; CAB65511.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR002086; Aldehyde_dehydr.
DR InterPro; IPR008972; Cupredoxin.
DR InterPro; IPR001799; Ephrin.
DR Pfam; PF00812; Ephrin; 1.
DR PRINTS; PR01347; EPHRIN.
DR ProDom; PD002533; Ephrin; 1.
DR PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; 1.
DR PROSITE; PS01299; EPHRIN; 1.
KW Signal.
FT SIGNAL 1 24 POTENTIAL.
SQ SEQUENCE 327 AA; 35913 MW; 4BB0FA39D4C22DCD CRC64;

Query Match 49.7%; Score 919; DB 13; Length 327;
Best Local Similarity 60.4%; Pred. No. 1.6e-63;
Matches 192; Conservative 30; Mismatches 82; Indels 14; Gaps 8;

Qy 25 VSGLSLEPVYWN SANKRFQ AEGGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLV 84
:| |||:|:||||:||||: ||||| ||||| |||||: | || || ||:|||||
Db 22 ISALS LDPIYWNSSNKRFEDETEGYVLYPQIGDRLDLLCPRSEPQGPFS SSPYEYKLYLV 81
Qy 85 GGAQG-RRCEAPPAPNLLLTCDRPDLDLRFITKFQEYSPNLWGHEFRSHHDYIIATSDG 143
| : | ||||| ||||| |||||:|||||:| |||||
Db 82 GTKEEMSSCSILRTPNLLLTCDRPSQDLRFITKFQEFSPNLWGHEFQSQRDYIIATSDG 141
Qy 144 TREGLES LQGGVCLTRGMKVLLRVGQSPRGGA VPRKPVSEMPMERDRGAHSL-EPGKEN 202
| :|:|:||||| |:||| |:|||| | ||:| | :| | :| |
Db 142 TMDGIETLQGGVCETKGMKVTLKVGQSPNGATPPRRPSS---AGKDSGISPSVNPDPIN 198
Qy 203 LPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMCWRRRRAKPSER 262
: | : : || | |||| :| ||||| |||| | | | :| |||:| | :|
Db 199 V-GETSGNATKTGENGPLPISHVPLVAGAAGGAALLLL-VFGVVGWVCHRRRQAKHSDTR 256
Qy 263 HPGPGSFGRGSLGLGGGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPV 322


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Db      190 GTNGKSSTTSPFVKDHSGSSTDG--SKAGHSSILGSEVALFAGIASGCIIFIVIIITLVV 247
QY      248 AMCWRRRRRAKPSESRRHPGPGSFGRGGSGLGLGGGGMGPREAEPGELGIALRGGGAADPPF 307
      :   ||| :   :|   |   :   |   :|| :: | ||   || |
Db      248 LLLKYRRRRHRKHSPQHNTTTLSTLATPKRSGNN----NGSEPSDIIIPLR---TADSVF 300
QY      308 CPHYEKVSGDYGHPVYIVQDGPPQSPNNIYYKV 340
      ||||| ||||| ||||| : |||| | |||| |
Db      301 CPHYEKVSGDYGHPVYIVQEMPPQSPANIYYKV 333

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RESULT 4

Q90Z33

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ID      Q90Z33      PRELIMINARY;      PRT;      341 AA.
AC      Q90Z33;
DT      01-DEC-2001 (TrEMBLrel. 19, Created)
DT      01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT      01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE      Ephrin B1.
GN      EFNBl.
OS      Brachydanio rerio (Zebrafish) (Danio rerio).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC      Cyprinidae; Danio.
OX      NCBI_TaxID=7955;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=21290827; PubMed=11397014;
RA      Chan J., Mably J.D., Serluca F.C., Chen J.N., Goldstein N.B.,
RA      Thomas M.C., Cleary J.A., Brennan C., Fishman M.C., Roberts T.M.;
RT      "Morphogenesis of prechordal plate and notochord requires intact
RT      eph/ephrin b signaling.";
RL      Dev. Biol. 234:470-482(2001).
DR      EMBL; AF375224; AAK64274.1; -.
DR      ZFIN; ZDB-GENE-010618-2; efnbl.
DR      GO; GO:0016020; C:membrane; IEA.
DR      InterPro; IPR008972; Cupredoxin.
DR      InterPro; IPR001799; Ephrin.
DR      Pfam; PF00812; Ephrin; 1.
DR      PRINTS; PR01347; EPHRIN.
DR      ProDom; PD002533; Ephrin; 1.
DR      PROSITE; PS01299; EPHRIN; 1.
SQ      SEQUENCE      341 AA;      37849 MW;      CB922F20E0D93E94 CRC64;

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Query Match      33.3%; Score 616; DB 13; Length 341;
Best Local Similarity 41.8%; Pred. No. 6e-40;
Matches 141; Conservative 49; Mismatches 109; Indels 38; Gaps 11;

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```

QY      24 LVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYL 83
      | : ||| | ||| | :| : | :||:||||:||||: | | |||||
Db      23 LPAAKSLESVVWNSQNPKFVSGKGLVIYPEIGDKLDIICPK----GDMGRP-YEFYKLYL 77
QY      84 VGGAQGRRCCEAPPAPNLLLTCDRDLRLFTIKFQEYSPNLWGHEFRSHHDYIIATSDG 143
      | | | | ||:||||:| :|:|||||:|||| | ||: :||| :||:|
Db      78 VKKEQAESCSTILDPNVLVTCNKPEKDIKFTIKFQEFSPNYMGLEFKRFTNYITSTNSG 137
QY      144 TREGLESQGGVCLTRGMKVLLRVGQSPRG-----GAVPRKPVSEMPMERDRGAAHSLEP 198

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      |   :   ||| ||:| | :|| |||:|||| | |   ||:|:|:| | | |||:
Db      86  ETCHVTKSDMLLLNCDKPDQDVKFTFKFQEFSPNLWGLEFLRGKDYHIISTSNSTFEGLD 145
QY      150  SLQGGVCLTRGMKVLLRVGQSPRGGAV----PRKPVSEMPMERDRGAAHSLEPGKENLPG 205
      :   ||| | : | :| ||||| | |   | :   : |   :|:   |||
Db      146  NHHGGVCRSKSMKLVLRVQSPTDSFSAKNHPTRNPPKYPENKDQNTF-----SKENDVS 200
QY      206  --DPTSNAISRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMCW-----RR 253
      |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
Db      201  QIDSMQNGESGGKSG-----ESVGSAGSDVALFAGV--ASGAVIFILIIIALVALLH 250
QY      254  RRAKPSESRRHPGPGSFGRGGSGLGLGGGGMGPREAEPGELGIALRGGAADPPFCPHYEK 313
      || :   : : |   |   |   |   |   |   |   |   |   |   |   |   |
Db      251  RRHQKHSAQCSGQLPLNTLPKRGSASGGSNNNGSEPSDIIFFPIRTSGSM---YCPHYEK 307
QY      314  VSGDYGHPVYIVQDGPQSPNNIYYKV 340
      ||||| ||||| ||||| : |||:| |||||
Db      308  VSGDYGHPVYIVQEMPPQNPNANIYYKV 334

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RESULT 6

Q9W6H9

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ID   Q9W6H9          PRELIMINARY;          PRT;    205 AA.
AC   Q9W6H9;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Ephrin-B2 (Fragment).
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97411149; PubMed=9259557;
RA   Smith A., Robinson V., Patel K., Wilkinson D.G.;
RT   "The EphA4 and EphB1 receptor tyrosine kinases and ephrin-B2 ligand
RT   regulate targeted migration of branchial neural crest cells.";
RL   Curr. Biol. 7:561-570(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20099673;
RA   Helbling P.M., Saulnier D.M., Robinson V., Christiansen J.H.,
RA   Wilkinson D.G., Brandli A.W.;
RT   "Comparative analysis of embryonic gene expression defines potential
RT   interaction sites for Xenopus EphB4 receptors with ephrin-B ligands.";
RL   Dev. Dyn. 216:361-373(1999).
DR   EMBL; AF128844; AAD32610.1; -.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR008972; Cupredoxin.
DR   InterPro; IPR001799; Ephrin.
DR   Pfam; PF00812; Ephrin; 1.
DR   ProDom; PD002533; Ephrin; 1.
FT   NON_TER      1      1
SQ   SEQUENCE      205 AA;  22256 MW;  7DEDD34277260C87 CRC64;

```

Query Match 18.4%; Score 340; DB 13; Length 205;
 Best Local Similarity 37.0%; Pred. No. 9.6e-19;
 Matches 84; Conservative 35; Mismatches 72; Indels 36; Gaps 7;

```

QY      128 EFRSHHDYIIATSDGTREGLESIQGGVCLTRGMKVLLRVGQSP-----RGGAVPRKPV 182
      ||: |||||:|:|: ||::: |||||:|: ||:|:| || | || : |:|
Db      1 EFQRDKDYIIISTNGSLEGVNDQEGGVCVTKAMKILMKVGQDPNFHNHRGASSTRRPDH 60

QY      183 EMPM--ERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240
      | : : | | : | :: | | | || | | : ::
Db      61 ESGTNGKSSTTSPHVNGPEGSSTEGKNAGHSSILGSEVAL-----FAGIASGSIIFIV 113

QY      241 GVAGAGGAMCWRRRRRAKPSESRRHPGPGSFGRGGSGLGLG-----GGGGMGPREAEPGEL 293
      : : ||| : : | : | | | | : || ::
Db      114 IIITLVVLLLYRRRRHRKHSPQHT-----TSLSLTLATPKRSGNNG---SEPSDI 161

QY      294 GIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPENIYYKV 340
      | || | : ||||| ||||| ||||| : |||| |||||
Db      162 IIPLR---TAEGVFCPHYEKVSGDYGHPVYIVQEMPPQSPANIYYKV 205
  
```

RESULT 7

Q9U3M2

```

ID   Q9U3M2          PRELIMINARY;          PRT;    237 AA.
AC   Q9U3M2;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   C43F9.8 protein.
GN   C43F9.8.
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Mortimore B.J.;
RL   Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99069613; PubMed=9851916;
RA   none;
RT   "Genome sequence of the nematode C.elegans: A platform for
RT   investigating biology.";
RL   Science 282:2012-2018(1998).
DR   EMBL; Z82262; CAB54195.1; -.
DR   PIR; T19914; T19914.
DR   WormPep; C43F9.8; CE23593.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR008972; Cupredoxin.
DR   InterPro; IPR001799; Ephrin.
DR   Pfam; PF00812; Ephrin; 1.
DR   PRINTS; PR01347; EPHRIN.
DR   ProDom; PD002533; Ephrin; 1.
SQ   SEQUENCE    237 AA;  26748 MW;  B9B2D9FCC71FE4FC CRC64;
  
```

Query Match 11.6%; Score 214.5; DB 5; Length 237;

Best Local Similarity 25.7%; Pred. No. 6.5e-09;
Matches 53; Conservative 41; Mismatches 83; Indels 29; Gaps 6;

```

QY      11 VRVGALLLLGVLGLVS-GLSLEPVYWNSANKRFQAEG-GYVLYPQIGDRDLDCPRARPP 68
      ::  :|| :  :  :  : | |:| |  :|: |||: : ||::
Db      1 MQIATFILLSLFPFIGWARKIPDINWISSNPIFDVSNTHVISVHIGDRVSIRCPKSD 60

QY      69 GPHSSPNYEFYKLYLVGGAQGRRCCEAPPAPNLLLTCDRDLRLRFTIKFQEYSPNLWGHE 128
      |  :|| :||: :  |  | |: |  ::  | |: ::|  ||
Db      61 G-----KYEYSYIYMVSDEEYDHCFL-SKPRLVGACDNQTINASINIVFRSFTPTPGGFE 114

QY      129 FRSHHDYIIA-----TSDGTREGLESIQGGVCLTRGMKVLLRVGQ 169
      |:  :|::|:  |||| |::: : |:| : ||:  |||
Db      115 FQPGKNYFLISKSEVDALIIYETANQIFPGTSDGTLEGIDRKKDGLCTAKQMKIKFEV 174

QY      170 SPRGGAVPRKPVSEMPMERDRGAH 195
      ||  |:  :  ::|| | ||
Db      175 DRGNIENPK--FAARTLKKDRDAEHS 198

```

RESULT 8

Q9U474

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ID   Q9U474          PRELIMINARY;          PRT;    279 AA.
AC   Q9U474;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   VAB-2 (Hypothetical protein Y37E11AR.6).
GN   VAB-2 OR Y37E11AR.6.
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=N2;
RX   MEDLINE=20084449; PubMed=10619431;
RA   Chin-Sang I.D., George S.E., Ding M., Moseley S.L., Lynch A.S.,
RA   Chisholm A.D.;
RT   "The ephrin VAB-2/EFN-1 functions in neuronal signaling to regulate
RT   epidermal morphogenesis in C. elegans.";
RL   Cell 99:781-790(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Bristol N2;
RX   MEDLINE=99069613; PubMed=9851916;
RA   None;
RT   "Genome sequence of the nematode C. elegans: a platform for
RT   investigating biology. The C. elegans Sequencing Consortium.";
RL   Science 282:2012-2018(1998).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Bristol N2;
RA   Miller N., Maggi L.;
RT   "The sequence of C. elegans cosmid Y37E11AR.";
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN   [4]

```


RP SEQUENCE FROM N.A.
 RC STRAIN=Berkeley;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
 RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkley;
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Dresnek L., Farfan D., Frise E.,
 RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
 RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
 RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
 RA Celniker S.;
 RL Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF216287; AAF28394.1; -.
 DR EMBL; AE003843; AAF59335.2; -.
 DR EMBL; BT005199; AAO61756.1; -.
 DR FlyBase; FBgn0040324; Ephrin.
 DR GO; GO:0016020; C:membrane; IEA.
 DR InterPro; IPR008972; Cupredoxin.

DR InterPro; IPR001799; Ephrin.
DR Pfam; PF00812; Ephrin; 1.
DR PRINTS; PR01347; EPHRIN.
DR ProDom; PD002533; Ephrin; 1.
SQ SEQUENCE 652 AA; 72302 MW; 5BA2F02F15964594 CRC64;

Query Match 9.8%; Score 182; DB 5; Length 652;
Best Local Similarity 22.9%; Pred. No. 7.2e-06;
Matches 88; Conservative 50; Mismatches 136; Indels 110; Gaps 18;

Qy 33 VYWNSANKRFQAEG-GYVLYPQIG-----DRLDLLCPRARPPGPHSSPNYEFYKLYLVG 85
::||::| |: : ::| |:: ::|| || : ||:| |
Db 219 MHWNTSNSIFRIDNTDHIIDVNKGNLAFEFQVHIICP-VYEPGTFENET-EKYIIYNVS 276

Qy 86 GAQGRRCCEAPPA-PNLLLTCDRDLRLRFTIKFQEYSPNLWGHEFRSHHDYIIATSDGT 144
: | | : ||:| : ||| |: ::| | || :||| |:|| :
Db 277 KVEYETCRITNADPRVIAICDKPQKLMFFTITFRPFTPQPGGLEFLPGNDYYFISTS--S 334

Qy 145 REGLESIQGGVCLTRGMKVLLRVGQSPRGGA VPRKPVSEMPMERDRGAAHSL-----EPG 199
:: | || | |||: :| :| :| | | : : :
Db 335 KDDLYRRIGGR CSTNNMKVVFKVCCAPEDNN-KTTALSNSKSVTDTGGAINVNIANNDDES 393

Qy 200 KENLPGDPTS NATSRGAEG-----PLPP-----P 223
| |: : |: | | |: | |
Db 394 HVNSHGNNIAIGTNIGINGGQIIGGPQSAGIPINPLSGNNNINGIPTTINSNIDQFNRI P 453

Qy 224 SMPAVAGAAGGLALLLLGVAGAGGAMCWRRRRAKPSERHPGPG-SFGRGGS LGLGGGGG 282
| : | | : |: | || : || : | | |||
Db 454 IQPNIIGNHVGTNAVGTGIVGGGGIIL-----TPGHAHGNNINMLQPGRGGI 499

Qy 283 MGPRAEAPG----ELGIALRG-----GGAADPPFCPHYEKVSGDYGH 320
| | || : || : | | ||| |
Db 500 NG---AYPGHHHIQTGIRINNVP TQHNYP SHKGNANSNINGNDDH---HHY NK-----H 547

Qy 321 PVYIVQD-----GPPQSPPNIY 337
| :|: : | | ||:
Db 548 PNEVVKNEELTYNSGAATSDGNIF 571

RESULT 10

Q98TZ1

ID Q98TZ1 PRELIMINARY; PRT; 202 AA.
AC Q98TZ1;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Ephrin-A6 (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Menzel P., Valencia F., Godement P., Dodelet V.C., Pasquale E.B.;
RT "Ephrin-A6, a new ligand for EphA receptors in the developing visual
RT system.";

DR ProDom; PD002533; Ephrin; 1.
 DR PROSITE; PS01299; EPHRIN; 1.
 DR PROSITE; PS00678; WD_REPEATS_1; 1.
 SQ SEQUENCE 205 AA; 23785 MW; 4FE9A6D94C1251A9 CRC64;

Query Match 9.1%; Score 168.5; DB 4; Length 205;
 Best Local Similarity 27.5%; Pred. No. 2.1e-05;
 Matches 52; Conservative 33; Mismatches 85; Indels 19; Gaps 7;

QY 18 LLGVLGLVSGLSLEPVYWNSANKRFQAGGYVLYPQIGDRLDLLCPRARPPGPHSSPN-- 75
 |||: :: |:|||:| :|: | | :: |: | :|::|| || :
 Db 8 LLGLCCSLAAADRHTVFWNSSNPKEFRNE-DYTIHVQLNDYVDIICPHYE---DHSVADAA 63

QY 76 YEFYKLYLVGGAQGRRCCEAPPAPNLLLTCDRDL---DLRFTIKFQEYSPNLWGHEFRSH 132
 | | |||| : : |: : | :|| : : ||| ::| | ||:
 Db 64 MEQYILYLVEHEEYQLCQPQSKDQVRWQCNRPQSAKHGPEKLSEKFQRFPTPLGKEFKEG 123

QY 133 HDYIIATSDGTREGLESQGGVCLTRGMKVLLRVGQSPRGGAVP--RKPVSEMPMERD- 189
 | || |: | || : | :: ||: | :: :: | |
 Db 124 HSYYYISKPIHQHEDR-----CLRLKVTVSGKITHSPQAHVNPQEKRLAADDPEVRVL 176

QY 190 RGAHSLEP 198
 ||| |
 Db 177 HSIHSAAP 185

RESULT 12

Q9D7K8

ID Q9D7K8 PRELIMINARY; PRT; 205 AA.
 AC Q9D7K8;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Adult male tongue cDNA, RIKEN full-length enriched library,
 DE clone:2310004J15, full insert sequence.
 GN EFNA1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Tongue;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzairelli J., Mombaerts P.,

RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 DR EMBL; AK009144; BAB26102.1; -.
 DR MGD; MGI:103236; Efnal.
 DR GO; GO:0016020; C:membrane; IEA.
 DR InterPro; IPR008972; Cupredoxin.
 DR InterPro; IPR001799; Ephrin.
 DR InterPro; IPR001680; WD40.
 DR Pfam; PF00812; Ephrin; 1.
 DR PRINTS; PR01347; EPHRIN.
 DR ProDom; PD002533; Ephrin; 1.
 DR PROSITE; PS01299; EPHRIN; 1.
 DR PROSITE; PS00678; WD_REPEATS_1; 1.
 SQ SEQUENCE 205 AA; 23772 MW; E37E55767459A4EC CRC64;

QY	18	LLGVLLGLVSGLSLEPVYWN	SANKRFQ	AEGGYVLYPQ	IGDRLLDLC	PRARPPGPHSSPNYE	77
		:	:	: :	:	:	:
Db	8	LLGLCCSLAAADRHIVFWN	SSNPKFREE	-D	YTVHVQLNDYLD	IICPHYEDDSV-ADAAME	65
QY	78	FYKLYLVGGAQ	GRRCEAPPAPN	LLLTCDR	PDL---	DLRFTIKFQ	EYSPNLWGHEFRSHHD
			:	:	:	:	:
Db	66	RYTLYMVEHQEY	VACQPQSKDQ	VRWNCNRP	SAKHGPEKLS	VKFQRF	TPFILGKEFKEGHS
			:	:	:	:	:
QY	135	YYIIATSDGT	TREGLES	LQGGVCL	TRGMKVLL	RVGQSPRGGAVPRK	179
			:	:		:	:
Db	126	YYYISKPIYHQE	-----	SQCLKLKVT	VNGKITHNP	QAHVNPQE	163
			:	:		:	:

RESULT 13

```
ID Q9CZS8 PRELIMINARY; PRT; 206 AA.
AC Q9CZS8;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 10 days embryo cDNA, RIKEN full-length enriched library,
DE clone:2610529M21, full insert sequence.
GN EFNA4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.
```

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 DR EMBL; AK012195; BAB28092.1; -.
 DR MGD; MGI:106643; Efna4.
 DR GO; GO:0016020; C:membrane; IEA.
 DR InterPro; IPR008972; Cupredoxin.
 DR InterPro; IPR001799; Ephrin.
 DR Pfam; PF00812; Ephrin; 1.
 DR PRINTS; PR01347; EPHRIN.
 DR ProDom; PD002533; Ephrin; 1.
 DR PROSITE; PS01299; EPHRIN; 1.
 SQ SEQUENCE 206 AA; 22859 MW; 675E32971D1C6EBC CRC64;

Query Match 8.8%; Score 163.5; DB 11; Length 206;
 Best Local Similarity 28.1%; Pred. No. 5.1e-05;
 Matches 61; Conservative 17; Mismatches 80; Indels 59; Gaps 10;

QY 32 PVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVGGAQGRR 91
 | : | | | : | | | | : | | | : | | : | | : | :
 Db 29 PIYWNSSNPRL-LRGDAVVELGFENDYLDIFCPHYESP GPPEGP--ETFALYIVDWSGYEA 85
 QY 92 CEAPPAPNL-LLTCDRPDL---DLRFTIKFQEYSPNLWGHEFRSHHDYIIATSDGTREG 147
 | | : | | : | | : | | : | | : | | : | | : |
 Db 86 CTAEGANSFQRWNC SMPFAPFSPVRFSEKIQRYPFPLGFEFLPGETYYYYISVPTPESPG 145
 QY 148 -LESLQGGVCLTRGMKVLLRVGQSPRGAVPRKPVSEMPMERDRGA AH-SLEPGKENLPG 205
 | | | | : | | : | | : | | : | | : | | : |
 Db 146 RCLRLQVSVCC-----KESGSSHESAHP-----VG 170
 QY 206 DPTSNATS--RGAEGPLPPPSMPAVAGAAGGLALLLL 240
 | : | | | | | | | | | | | | | | | | | |
 Db 171 SPGESGTSGWRGGHAPSP-----LCLLLL 194

RESULT 14

Q9N178

ID Q9N178 PRELIMINARY; PRT; 675 AA.
 AC Q9N178;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

Db 475 PP-GPAGIATK 484

RESULT 15

O93431

ID O93431 PRELIMINARY; PRT; 229 AA.
AC O93431;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Ephrin A-L1.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Durbin L., Brennan C.H., Shiomi K., Cooke J.;
RT "Eph signalling is required for segmentation and differentiation of
RT the somites."
RL Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AJ006838; CAA07264.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR008972; Cupredoxin.
DR InterPro; IPR001799; Ephrin.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00812; Ephrin; 1.
DR PRINTS; PR01347; EPHRIN.
DR ProDom; PD002533; Ephrin; 1.
DR PROSITE; PS01299; EPHRIN; 1.
DR PROSITE; PS00290; IG_MHC; 1.
SQ SEQUENCE 229 AA; 26115 MW; 8684462F67AF6F5C CRC64;

Query Match 8.4%; Score 155; DB 13; Length 229;

Best Local Similarity 27.2%; Pred. No. 0.00026;

Matches 56; Conservative 23; Mismatches 93; Indels 34; Gaps 7;

Qy 33 VYWNSANKRFQAEAGGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVGGAQGRRRC 92
| | | | | : | : : | | | : | | : | | : |
Db 25 VYWNSTNANFLWD-DYTVDVIRINDYLDIICPH-YAHGEIASQEAERYVLYMVELEDYENC 82

Qy 93 EAPPAPNLLLTCDR---PDLDLRFTIKFQEYSPNLWGHEFRSHHDYIIATSDGTREGLE 149
: | | | | : | : | | : | | | | | : :
Db 83 KPHSFDQLRWECSPRFAPHAPEKFSEKFQRFPTFTLGKEFRQGESYYYYIS-----K 133

Qy 150 SL--QGGVCLTRGMKVLLRVGQSPRGGA VPRKPVSEMPMERDRGAHSLPGKENLPGDP 207
| | | | : | : | | : | : | : | : |
Db 134 PLHHHGQECLRLKVDVV-----GPHGSKNKKKMVEKVEEIEGKMAAGGVHNPSNRLPADD 188

Qy 208 TSNATSRGAEGPLPPPSMPAVAGAAG 233
| : | | : |
Db 189 -----PIAMIPVVQRSVG 201

Search completed: September 15, 2004, 12:39:13

Job time : 66.8616 secs

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OM protein - protein search, using sw model

Run on: September 15, 2004, 12:22:15 ; Search time 13.2579 Seconds
(without alignments)
1335.348 Million cell updates/sec

Title: US-10-021-121-4
Perfect score: 1850
Sequence: 1 MGPPHSGPGGVRVGALLLLG.....PVYIVQDGPPQSPNNIYYKV 340

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	1850	100.0	340	1	EFB3_HUMAN	Q15768 homo sapien
2	1780	96.2	340	1	EFB3_MOUSE	O35393 mus musculu
3	637.5	34.5	336	1	EFB2_MOUSE	P52800 mus musculu
4	632	34.2	346	1	EFB1_HUMAN	P98172 homo sapien
5	629.5	34.0	333	1	EFB2_HUMAN	P52799 homo sapien
6	628	33.9	334	1	EFB1_CHICK	O73612 gallus gall
7	626.5	33.9	332	1	EFB2_BRARE	O73874 brachydanio
8	613.5	33.2	345	1	EFB1_MOUSE	P52795 mus musculu
9	608.5	32.9	345	1	EFB1_RAT	P52796 rattus norv
10	600	32.4	327	1	EFB1_XENLA	O13097 xenopus lae
11	185	10.0	195	1	EFA2_BRARE	P79727 brachydanio
12	179	9.7	238	1	EFA3_HUMAN	P52797 homo sapien
13	176	9.5	209	1	EFA2_MOUSE	P52801 mus musculu
14	175.5	9.5	213	1	EFA2_HUMAN	O43921 homo sapien
15	172	9.3	200	1	EFA2_CHICK	P52802 gallus gall
16	170.5	9.2	228	1	EFA5_CHICK	P52804 gallus gall
17	169.5	9.2	201	1	EFA4_HUMAN	P52798 homo sapien

18	169.5	9.2	228	1	EFA5_BRARE	P79728	brachydanio
19	167.5	9.1	216	1	EFA1_XENLA	P52794	xenopus lae
20	167.5	9.1	228	1	EFA5_HUMAN	P52803	homo sapien
21	167.5	9.1	228	1	EFA5_MOUSE	O08543	mus musculu
22	167.5	9.1	228	1	EFA5_RAT	P97605	rattus norv
23	166	9.0	205	1	EFA1_HUMAN	P20827	homo sapien
24	162.5	8.8	205	1	EFA1_RAT	P97553	rattus norv
25	161	8.7	205	1	EFA1_MOUSE	P52793	mus musculu
26	160.5	8.7	206	1	EFA4_MOUSE	O08542	mus musculu
27	159	8.6	680	1	CA1A_MOUSE	Q05306	mus musculu
28	154.5	8.4	1049	1	CA13_BOVIN	P04258	bos taurus
29	151.5	8.2	301	1	CC02_CAEEL	P17656	caenorhabdi
30	148.5	8.0	1670	1	CA34_HUMAN	Q01955	homo sapien
31	146.5	7.9	1774	1	CA1H_MOUSE	P39061	mus musculu
32	146	7.9	1027	1	CAFF_RIFPA	P30754	riftia pach
33	145	7.8	674	1	CA1A_BOVIN	P23206	bos taurus
34	145	7.8	1745	1	CA35_HUMAN	P25940	homo sapien
35	144.5	7.8	1516	1	CA1H_HUMAN	P39060	homo sapien
36	144	7.8	675	1	CA39_CHICK	P32017	gallus gall
37	144	7.8	921	1	CA19_HUMAN	P20849	homo sapien
38	143	7.7	674	1	CA1A_CHICK	P08125	gallus gall
39	142.5	7.7	1496	1	CA25_HUMAN	P05997	homo sapien
40	142	7.7	744	1	CA18_HUMAN	P27658	homo sapien
41	142	7.7	1029	1	CA26_MOUSE	Q02788	mus musculu
42	142	7.7	1763	1	CA24_ASCSU	P27393	ascaris suu
43	141.5	7.6	1466	1	CA13_HUMAN	P02461	homo sapien
44	141	7.6	744	1	CA18_RABIT	P14282	oryctolagus
45	140.5	7.6	743	1	CA18_MOUSE	Q00780	mus musculu

ALIGNMENTS

RESULT 1

EFB3_HUMAN

ID EFB3_HUMAN STANDARD; PRT; 340 AA.
AC Q15768; O00680; Q8TBH7; Q92875;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Ephrin-B3 precursor (EPH-related receptor tyrosine kinase ligand 8)
DE (LERK-8) (EPH-related receptor transmembrane ligand ELK-L3).
GN EFNB3 OR EPLG8 OR LERK8.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Cerretti D.P.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=97271551; PubMed=9126477;
RA Tang X.X., Pleasure D.E., Ikegaki N.;
RT "cDNA cloning, chromosomal localization, and expression pattern of

RT EPLG8, a new member of the EPLG gene family encoding ligands of EPH-
RT related protein-tyrosine kinase receptors.";
RL Genomics 41:17-24(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain cortex;
RX MEDLINE=96404527; PubMed=8808709;
RA Gale N.W., Flenniken A., Compton D.C., Jenkins N.A., Copeland N.G.,
RA Gilbert D.J., Davis S., Wilkinson D.G., Yancopoulos G.D.;
RT "Elk-L3, a novel transmembrane ligand for the Eph family of receptor
RT tyrosine kinases, expressed in embryonic floor plate, roof plate and
RT hindbrain segments.";
RL Oncogene 13:1343-1352(1996).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: May play a pivotal role in forebrain function. Binds to,
CC and induce the collapse of, commissural axons/growth cones in
CC vitro. May play a role in constraining the orientation of
CC longitudinally projecting axons (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: Highly expressed in brain; expressed in
CC embryonic floor plate, roof plate and hindbrain segments.
CC -!- SIMILARITY: Belongs to the ephrin family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U57001; AAB05170.1; -.
DR EMBL; U66406; AAC51203.1; -.
DR EMBL; U62775; AAC50707.1; -.

DR EMBL; BC022499; AAH22499.1; -.
 DR EMBL; BC042944; AAH42944.1; -.
 DR Genew; HGNC:3228; EFNB3.
 DR MIM; 602297; -.
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.
 DR GO; GO:0005005; F:transmembrane-ephrin receptor activity; TAS.
 DR GO; GO:0007267; P:cell-cell signaling; TAS.
 DR GO; GO:0007399; P:neurogenesis; TAS.
 DR InterPro; IPR008972; Cupredoxin.
 DR InterPro; IPR001799; Ephrin.
 DR Pfam; PF00812; Ephrin; 1.
 DR PRINTS; PR01347; EPHRIN.
 DR ProDom; PD002533; Ephrin; 1.
 DR PROSITE; PS01299; EPHRIN; 1.
 KW Developmental protein; Neurogenesis; Transmembrane; Glycoprotein;
 KW Signal; Polymorphism.
 FT SIGNAL 1 27 POTENTIAL.
 FT CHAIN 28 340 EPHRIN-B3.
 FT DOMAIN 28 226 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 227 247 POTENTIAL.
 FT DOMAIN 248 340 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 338 340 PDZ RECOGNITION MOTIF (POTENTIAL).
 FT DISULFID 62 104 BY SIMILARITY.
 FT DISULFID 92 156 BY SIMILARITY.
 FT CARBOHYD 210 210 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARIANT 166 166 R -> Q.
 FT /FTid=VAR_002356.
 SQ SEQUENCE 340 AA; 35834 MW; EDFF2A23C2FDE79F CRC64;

Query Match 100.0%; Score 1850; DB 1; Length 340;
 Best Local Similarity 100.0%; Pred. No. 1.3e-112;
 Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGPPHSGPGGVRVGALLLLGLVGLVSGLSLEPVYWNSANKRFQAEAGGYVLYPQIGDRLDL 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 MGPPHSGPGGVRVGALLLLGLVGLVSGLSLEPVYWNSANKRFQAEAGGYVLYPQIGDRLDL 60
 QY 61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120
 QY 121 SPNLWGHEFRSHHDYIIATSDGTREGLESQGQVCLTRGMKVLLRVGQSPRGGAVPRKP 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 121 SPNLWGHEFRSHHDYIIATSDGTREGLESQGQVCLTRGMKVLLRVGQSPRGGAVPRKP 180
 QY 181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNAATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNAATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240
 QY 241 GVAGAGGAMCWRRRRRAKPSERHPGPGSFGRGGSGLGLGGGGMGPREAEPGELGIALRGG 300
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 241 GVAGAGGAMCWRRRRRAKPSERHPGPGSFGRGGSGLGLGGGGMGPREAEPGELGIALRGG 300
 QY 301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYYKV 340
 ||||||||||||||||||||||||||||||||||||||||||||
 Db 301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYYKV 340

RESULT 2

EFB3_MOUSE

ID EFB3_MOUSE STANDARD; PRT; 340 AA.
AC O35393;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Ephrin-B3 precursor.
GN EFNB3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=98143367; PubMed=9484836;
RA Bergemann A.D., Zhang L., Chiang M.-K., Brambilla R., Klein R.,
RA Flanagan J.G.;
RT "Ephrin-B3, a ligand for the receptor EphB3, expressed at the midline
RT of the developing neural tube."
RL Oncogene 16:471-480(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP FUNCTION.
RX MEDLINE=20171264; PubMed=10704386;
RA Imondi R., Wideman C., Kaprielian Z.;
RT "Complementary expression of transmembrane ephrins and their receptors
RT in the mouse spinal cord: a possible role in constraining the
RT orientation of longitudinally projecting axons."
RL Development 127:1397-1410(2000).
CC -!- FUNCTION: May play a pivotal role in forebrain function. Binds to,
CC and induce the collapse of, commissural axons/growth cones in

```

CC      vitro. May play a role in constraining the orientation of
CC      longitudinally projecting axons.
CC      -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC      -!- TISSUE SPECIFICITY: Expressed on lateral floor plate cells,
CC      specifically on commissural axon segments that have passed through
CC      the floor plate. Expressed in cells of the retinal ganglion cell
CC      layer during retinal axon guidance to the optic disk.
CC      -!- DEVELOPMENTAL STAGE: Expressed in the floor plate throughout the
CC      period of commissural axon pathfinding.
CC      -!- SIMILARITY: Belongs to the ephrin family.
CC
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; AF025288; AAC53537.1; -.
DR      EMBL; BC052001; AAH52001.1; -.
DR      EMBL; BC058617; AAH58617.1; -.
DR      MGD; MGI:109196; Efnb3.
DR      GO; GO:0007628; P:adult walking behavior; IMP.
DR      GO; GO:0007411; P:axon guidance; IMP.
DR      InterPro; IPR008972; Cupredoxin.
DR      InterPro; IPR001799; Ephrin.
DR      Pfam; PF00812; Ephrin; 1.
DR      PRINTS; PR01347; EPHRIN.
DR      ProDom; PD002533; Ephrin; 1.
DR      PROSITE; PS01299; EPHRIN; 1.
KW      Developmental protein; Neurogenesis; Transmembrane; Glycoprotein;
KW      Signal.
FT      SIGNAL          1      27      POTENTIAL.
FT      CHAIN           28     340     EPHRIN-B3.
FT      DOMAIN          28     227     EXTRACELLULAR (POTENTIAL).
FT      TRANSMEM        228     248     POTENTIAL.
FT      DOMAIN          249     340     CYTOPLASMIC (POTENTIAL).
FT      DOMAIN          338     340     PDZ RECOGNITION MOTIF (POTENTIAL).
FT      DISULFID        62     104     BY SIMILARITY.
FT      DISULFID        92     156     BY SIMILARITY.
FT      CARBOHYD        210     210     N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ      SEQUENCE       340 AA;  35884 MW;  52F3D58FD209A6B8 CRC64;

Query Match          96.2%; Score 1780; DB 1; Length 340;
Best Local Similarity 95.6%; Pred. No. 4.3e-108;
Matches 325; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY      1 MGPPHSGPGGVVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60
      || || |||||:||||||| |||||||||||||||||||||||||||||||||||
Db      1 MGAPHFGPGGVQVGALLLLGFAGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60

QY      61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCAPPAPNLLLTCDRPDLDLRFTIKFQEY 120
      |||||||||||||:||||||| |||||||||||||||||||||||||||||||
Db      61 LCPRARPPGPHSSPSYEFYKLYLVEGAQGRRCAPPAPNLLLTCDRPDLDLRFTIKFQEY 120

QY      121 SPNLWGHEFRSHHDYIIATSDGTREGLESIQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180

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      |||
Db      121 SPNLWGHEFRSHHDYIIATSDGTREGLES LQGGVCLTRGMKVLLRVGQSPRGGA VPRKP 180
QY      181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240
      |||
Db      181 VSEMPMERDRGAAHSAEPGRDTIPGDPSSNATSRGAEGPLPPPSMPAVAGAAGGMALLLL 240
QY      241 GVAGAGGAMCWRRRRRAKPSERHPGPGSFGRGGS LGLGGGGGMGPRAEPGELGIALRGG 300
      |||
Db      241 GVAGAGGAMCWRRRRRAKPSERHPGPGSFGRGGS LGLGGGGGMGPRAEPGELGIALRGG 300
QY      301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYYKV 340
      |
Db      301 GTADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYYKV 340

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RESULT 3

EFB2_MOUSE

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ID      EFB2_MOUSE      STANDARD;      PRT;      336 AA.
AC      P52800;
DT      01-OCT-1996 (Rel. 34, Created)
DT      01-OCT-1996 (Rel. 34, Last sequence update)
DT      15-MAR-2004 (Rel. 43, Last annotation update)
DE      Ephrin-B2 precursor (EPH-related receptor tyrosine kinase ligand 5)
DE      (LERK-5) (HTK ligand) (HTK-L) (ELF-2).
GN      EFN2 OR EPLG5 OR LERK5 OR HTKL OR ELF2 OR EPL5.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=96145238; PubMed=8559144;
RA      Cerretti D.P., Vanden Bos T., Nelson N., Kozlosky C.J., Reddy P.,
RA      Maraskovsky E., Park L.S., Lyman S.D., Copeland N.G.,
RA      Gilbert D.J., Jenkins N.A., Fletcher R.A.;
RT      "Isolation of LERK-5: a ligand of the eph-related receptor tyrosine
RT      kinases.";
RL      Mol. Immunol. 32:1197-1205(1995).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      STRAIN=CB57BL/6J X SJL/J;
RX      MEDLINE=95199254; PubMed=7534404;
RA      Bennett B.D., Zeigler F.C., Gu Q., Fendly B., Goddard A.D.,
RA      Gillett N., Matthews W.;
RT      "Molecular Cloning of a ligand for the EPH-related receptor protein-
RT      tyrosine kinase Htk.";
RL      Proc. Natl. Acad. Sci. U.S.A. 92:1866-1870(1995).
RN      [3]
RP      SEQUENCE FROM N.A.
RC      STRAIN=ICR; TISSUE=Brain;
RX      MEDLINE=95379837; PubMed=7651410;
RA      Bergemann A.D., Cheng H.J., Brambilla R., Klein R., Flanagan J.G.;
RT      "ELF-2, a new member of the Eph ligand family, is segmentally
RT      expressed in mouse embryos in the region of the hindbrain and newly
RT      forming somites.";
RL      Mol. Cell. Biol. 15:4921-4929(1995).

```

RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RP FUNCTION.
 RX MEDLINE=20171264; PubMed=10704386;
 RA Imondi R., Wideman C., Kaprielian Z.;
 RT "Complementary expression of transmembrane ephrins and their receptors
 RT in the mouse spinal cord: a possible role in constraining the
 RT orientation of longitudinally projecting axons.";
 RL Development 127:1397-1410(2000).
 RN [6]
 RP X-RAY CRYSTALLOGRAPHY (1.92 ANGSTROMS) OF 30-170.
 RX MEDLINE=21563306; PubMed=11703926;
 RA Toth J., Cutforth T., Gelinas A.D., Bethoney K.A., Bard J.,
 RA Harrison C.J.;
 RT "Crystal structure of an ephrin ectodomain.";
 RL Dev. Cell 1:83-92(2001).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 31-168 IN COMPLEX WITH
 RP EPHB2.
 RX MEDLINE=21638766; PubMed=11780069;
 RA Himanen J.-P., Rajashankar K.R., Lackmann M., Cowan C.A.,
 RA Henkemeyer M., Nikolov D.B.;
 RT "Crystal structure of an Eph receptor-ephrin complex.";
 RL Nature 414:933-938(2001).
 CC -!- FUNCTION: Binds to the receptor tyrosine kinases EPHB2 and EPHB4.
 CC May play a role in constraining the orientation of longitudinally
 CC projecting axons.
 CC -!- SUBUNIT: Binds to the receptor tyrosine kinase EPHB4.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- TISSUE SPECIFICITY: Expressed on lateral floor plate cells,
 CC specifically on commissural axon segments that have passed through
 CC the floor plate. Expressed in cells of the retinal ganglion cell
 CC layer during retinal axon guidance to the optic disk.
 CC -!- DEVELOPMENTAL STAGE: Expressed in the floor plate throughout the

CC period of commissural axon pathfinding.
 CC -!- PTM: Inducible phosphorylation of tyrosine residues in the
 CC cytoplasmic domain (By similarity).
 CC -!- SIMILARITY: Belongs to the ephrin family.
 CC -----
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 CC -----
 DR EMBL; U16819; AAA99708.1; -.
 DR EMBL; L38847; AAC42052.1; -.
 DR EMBL; U30244; AAA82934.1; -.
 DR EMBL; BC057009; AAH57009.1; -.
 DR PIR; I49766; I49766.
 DR PDB; 1IKO; 15-MAY-02.
 DR PDB; 1KGY; 28-MAY-02.
 DR MGD; MGI:105097; Efnb2.
 DR InterPro; IPR008972; Cupredoxin.
 DR InterPro; IPR001799; Ephrin.
 DR Pfam; PF00812; Ephrin; 1.
 DR PRINTS; PR01347; EPHRIN.
 DR ProDom; PD002533; Ephrin; 1.
 DR PROSITE; PS01299; EPHRIN; 1.
 KW Developmental protein; Neurogenesis; Transmembrane; Glycoprotein;
 KW Signal; Phosphorylation; 3D-structure.
 FT SIGNAL 1 28 POTENTIAL.
 FT CHAIN 29 336 EPHRIN-B2.
 FT DOMAIN 29 232 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 233 253 POTENTIAL.
 FT DOMAIN 254 336 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 334 336 PDZ RECOGNITION MOTIF (POTENTIAL).
 FT DISULFID 65 104
 FT DISULFID 92 156
 FT CARBOHYD 39 39 N-LINKED (GLCNAC. . .).
 FT CARBOHYD 142 142 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 3 4 MISSING (IN REF. 3).
 FT CONFLICT 177 177 A -> T (IN REF. 1).
 SQ SEQUENCE 336 AA; 37202 MW; D08894996E399554 CRC64;

Query Match 34.5%; Score 637.5; DB 1; Length 336;
 Best Local Similarity 42.1%; Pred. No. 1.9e-34;
 Matches 139; Conservative 49; Mismatches 129; Indels 13; Gaps 5;

QY 14 GALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSS 73
 | |::| : : |||:||||:| :| | |||||:|:::|: :
 Db 17 GLLMVLCRTAISRSIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV 73
 QY 74 PNYEFYKLYLVGGAQGRRCAPPAPNLLLTCDRDLRFTIKFQEYSPNLWGHEFRSHH 133
 ||::|:|:| | || || | ||| |:|:|||||:|:|||| |:: :
 Db 74 GQYEEYKVYMVVDKDQADRCTIKKENTPLNLCARPDQDVKFTIKFQEYSPNLWGLEFQKNK 133
 QY 134 DYYIIATSDGTREGLESLOGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR 190
 ||||:|:|:|: |||:: :||| || |:|:|:| | | | :|

Db 134 DYYIIISTSNGLSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSARNHGPTRRPELEAGTN 193

QY 191 GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC 250
| : : | : || | : : : | : || | | : : : :

Db 194 GRSSTTSPFVKPNPGSSTDGNSAGHSIGNLLGSEVALFAGIASGCIIFIVIIITLVVLLL 253

QY 251 WRRRRRAKPSESRRHPGPGSFRGGSLGLGGGGMGPREAEPGELGIALRGGAADPPFCPH 310
||| : : | | : || : || : : | | || |||

Db 254 KYRRHRKHSPQHTTTLSLSTLATPKRGNN---NGSEPSDVIPLR---TADSVFCPH 306

QY 311 YEKVSGDYGHPVYIVQDGPPQSPNIIYKV 340
||||||| : |||| |||||

Db 307 YEKVSGDYGHPVYIVQEMPQSPANIIYKV 336

RESULT 4

EFB1_HUMAN

ID EFB1_HUMAN STANDARD; PRT; 346 AA.

AC P98172;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Ephrin-B1 precursor (EPH-related receptor tyrosine kinase ligand 2)

DE (LERK-2) (ELK ligand) (ELK-L).

GN EFNBI OR EPLG2 OR LERK2 OR EFL-3.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Placenta;

RX MEDLINE=94349923; PubMed=8070404;

RA Beckmann M.P., Cerretti D.P., Baum P., Vanden Bos T., James L.,

RA Farrah T., Kozlosky C., Hollingsworth T., Shilling H., Maraskovsky E.,

RA Fletcher F.A., Lhotak V., Pawson T., Lyman S.D.;

RT "Molecular characterization of a family of ligands for eph-related

RT tyrosine kinase receptors.";

RL EMBO J. 13:3757-3762(1994).

RN [2]

RP SEQUENCE FROM N.A.

RA Davis S., Gale N.W., Aldrich T.H., Maisonpierre P.C., Lhotak V.,

RA Pawson T., Goldfarb M., Yancopoulos G.D.;

RL Submitted (NOV-1994) to the EMBL/GenBank/DDBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RA Fletcher F.A., Huebner K., Shaffer L.G., Monaco A., Mueller U.,

RA Kozlosky C., Druck T., Simoneaux D.K., Fairweather N., Chelly J.,

RA Cerretti D.P., Belmont J.W., Beckmann M.P., Lyman S.D.;

RL Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.

RN [4]

RP SEQUENCE FROM N.A.

RA Howden P.;

RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.

RN [5]

RP SEQUENCE FROM N.A.

RC TISSUE=Eye, and Skin;

RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- FUNCTION: Binds to the receptor tyrosine kinases EPHB1 and EPHA1.
 CC Binds to, and induce the collapse of, commissural axons/growth
 CC cones in vitro. May play a role in constraining the orientation of
 CC longitudinally projecting axons (By similarity).
 CC -!- SUBUNIT: Binds GRIP1 and GRIP2.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- TISSUE SPECIFICITY: Heart, placenta, lung, liver, skeletal muscle,
 CC kidney, pancreas.
 CC -!- INDUCTION: By TNF-alpha.
 CC -!- PTM: Inducible phosphorylation of tyrosine residues in the
 CC cytoplasmic domain (By similarity).
 CC -!- SIMILARITY: Belongs to the ephrin family.
 CC -----
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 CC -----
 DR EMBL; U09304; AAA53093.1; -.
 DR EMBL; L37361; AAA52369.1; -.
 DR EMBL; U09303; AAB41127.1; -.
 DR EMBL; AL136092; -; NOT_ANNOTATED_CDS.
 DR EMBL; BC016649; AAH16649.1; -.
 DR EMBL; BC052979; AAH52979.1; -.
 DR PIR; S46993; S46993.
 DR Genew; HGNC:3226; EFNBL1.
 DR MIM; 300035; -.
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.
 DR GO; GO:0005625; C:soluble fraction; TAS.
 DR GO; GO:0005108; F:transmembrane ephrin; TAS.
 DR GO; GO:0007155; P:cell adhesion; TAS.
 DR GO; GO:0007267; P:cell-cell signaling; TAS.
 DR InterPro; IPR008972; Cupredoxin.

DR InterPro; IPR001799; Ephrin.
 DR Pfam; PF00812; Ephrin; 1.
 DR PRINTS; PR01347; EPHRIN.
 DR ProDom; PD002533; Ephrin; 1.
 DR PROSITE; PS01299; EPHRIN; 1.
 KW Developmental protein; Neurogenesis; Transmembrane; Glycoprotein;
 KW Signal; Phosphorylation.
 FT SIGNAL 1 24 POTENTIAL.
 FT CHAIN 25 346 EPHRIN-B1.
 FT DOMAIN 25 237 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 238 258 POTENTIAL.
 FT DOMAIN 259 346 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 344 346 PDZ RECOGNITION MOTIF (POTENTIAL).
 FT DISULFID 64 101 BY SIMILARITY.
 FT DISULFID 89 153 BY SIMILARITY.
 FT CARBOHYD 139 139 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 346 AA; 38006 MW; 473DD2F1A5BF89DE CRC64;

Query Match 34.2%; Score 632; DB 1; Length 346;
 Best Local Similarity 39.5%; Pred. No. 4.4e-34;
 Matches 145; Conservative 48; Mismatches 116; Indels 58; Gaps 9;

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Qy      8 PGGVRVGALLLLGVLGLVSGL-----SLEPVYWNSANKRFQAEGGYVLYPQIGDRDL 61
      ||  :| |:  : |  :||| |:| |:| : | :||:|:|:|:|:
Db      4 PGQRWLKGWLVAMVWALCRLATPLAKNLEPVSWSLNPKFLSGKGLVIYPKIGDKLDII 63

Qy     62 CPRARPPGPHSSPNYEFYKLYLVGGAQGRRCCEAPPAPNLLLTCDRDPDLDLRETIKFQEYS 121
      |||  |  :|:|:|:|  |  |  :|:|:|:|:|:|:|:|:|:|
Db     64 CPRAEAGRP-----YEYKLYLVRPEQAAACSTVLDPNVLVTCNRPEQEIRFTIKFQEFS 118

Qy    122 PNLWGHEFRSHHDYIIATSDGTREGLESLOGGVCLTRGMKVLLRVGQSPRGGAVERPKPV 181
      ||  | |:| :|:|:|:| :|:|:|:| :|:|:|:| :|:|:|:| :|:|:|:|
Db    119 PNYMGLEFKKHHDYITSTSNGLSLEGLNREGGVCRTRTMKIIMKVGQDPNAVTPPEQLTT 178

Qy    182 SEMPMERDRGAHSLE-PGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLA---- 236
      |  |  |  : : ||  ||  :  |  |  :|:|:|:|
Db    179 SRPSKEADNTVKMATQAPGSRGSLGSDGKHETVNTQEEKSGP-----GASGGSSGDPD 231

Qy    237 -----LLLLGVAGAGGA-----MCWRRRRRAKPSESRRHPGPGSFGRGGSLSGL 277
      : |  |||  : |:| | :|  | :| |
Db    232 GFFNSKVALFAAVGAGCVIFLLIIIFLTVLLKLKRHRKHTQQ-----RAAALSL 282

Qy    278 ----GGGGMGPREAEPGELGIALRGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP 333
      || |  || : : ||  :  :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db    283 STLASPKGGSGTAGTEPSDIIPLR---TTENNYCPHYEKVSGDYGHPVYIVQEMPQSP 339

Qy    334 PNIIYKV 340
      |||||
Db    340 ANIIYKV 346

```

RESULT 5

EFB2_HUMAN

ID EFB2_HUMAN STANDARD; PRT; 333 AA.

AC P52799;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Ephrin-B2 precursor (EPH-related receptor tyrosine kinase ligand 5)
 DE (LERK-5) (HTK ligand) (HTK-L).
 GN EFNB2 OR EPLG5 OR LERK5 OR HTKL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=96145238; PubMed=8559144;
 RA Cerretti D.P., Vanden Bos T., Nelson N., Kozlosky C.J., Reddy P.,
 RA Maraskovsky E., Park L.S., Lyman S.D., Copeland N.G., Gilbert D.J.,
 RA Jenkins N.A., Fletcher R.A.;
 RT "Isolation of LERK-5: a ligand of the eph-related receptor tyrosine
 RT kinases.";
 RL Mol. Immunol. 32:1197-1205(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=95199254; PubMed=7534404;
 RA Bennett B.D., Zeigler F.C., Gu Q., Fendly B., Goddard A.D.,
 RA Gillett N., Matthews W.;
 RT "Molecular cloning of a ligand for the EPH-related receptor protein-
 RT tyrosine kinase Htk.";
 RL Proc. Natl. Acad. Sci. U.S.A. 92:1866-1870(1995).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98192220; PubMed=9533549;
 RA Vogt T., Stolz W., Welsh J., Jung B., Kerbel R.S., Kobayashi H.,
 RA Landthaler M., McClelland M.;
 RT "Overexpression of Lerk-5/Eplg5 messenger RNA: a novel marker for
 RT increased tumorigenicity and metastatic potential in human malignant
 RT melanomas.";
 RL Clin. Cancer Res. 4:791-797(1998).
 CC -!- FUNCTION: Binds to the receptor tyrosine kinases EPHB4 and EPHA3.
 CC May play a role in constraining the orientation of longitudinally
 CC projecting axons (By similarity).
 CC -!- SUBUNIT: Binds to the receptor tyrosine kinases EPHB4 and EPHA3.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- TISSUE SPECIFICITY: Lung and kidney.
 CC -!- PTM: Inducible phosphorylation of tyrosine residues in the
 CC cytoplasmic domain (By similarity).
 CC -!- SIMILARITY: Belongs to the ephrin family.
 CC -----
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 CC -----
 DR EMBL; U16797; AAA99707.1; -.
 DR EMBL; L38734; AAC41752.1; -.
 DR EMBL; U81262; AAD03786.1; -.

```

DR      PIR; I84743; I84743.
DR      Genew; HGNC:3227; EFNB2.
DR      MIM; 600527; -.
DR      GO; GO:0005887; C:integral to plasma membrane; TAS.
DR      GO; GO:0005106; F:ephrin; TAS.
DR      GO; GO:0005108; F:transmembrane ephrin; TAS.
DR      GO; GO:0007267; P:cell-cell signaling; TAS.
DR      GO; GO:0007397; P:histogenesis and organogenesis; TAS.
DR      InterPro; IPR008972; Cupredoxin.
DR      InterPro; IPR001799; Ephrin.
DR      Pfam; PF00812; Ephrin; 1.
DR      PRINTS; PR01347; EPHRIN.
DR      ProDom; PD002533; Ephrin; 1.
DR      PROSITE; PS01299; EPHRIN; 1.
KW      Developmental protein; Neurogenesis; Transmembrane; Glycoprotein;
KW      Signal; Phosphorylation.
FT      SIGNAL      1      27      POTENTIAL.
FT      CHAIN      28      333      EPHRIN-B2.
FT      DOMAIN      28      229      EXTRACELLULAR (POTENTIAL).
FT      TRANSMEM      230      250      POTENTIAL.
FT      DOMAIN      251      333      CYTOPLASMIC (POTENTIAL).
FT      DOMAIN      331      333      PDZ RECOGNITION MOTIF (POTENTIAL).
FT      DISULFID      62      101      BY SIMILARITY.
FT      DISULFID      89      153      BY SIMILARITY.
FT      CARBOHYD      36      36      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD      139      139      N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ      SEQUENCE      333 AA;  36923 MW;  6D9932A632626AEA CRC64;

```

QY	14	GALLLLGLVGLSVGLSLEPVIWNSANKRFQAEGGVLYLPQIGDRDLLCPRARPPGPHSS	73
Db	14	GVLMLCRLTAISKSIIVLEPIYWNSSNSKFLPGQGVLVLYPQIGDKLDIICPKV---DSKTV	70
QY	74	PNYEFYKLYLVGGAQGRRCCEAPPAPNLLLTCDRDLRLFTIKFQEYSPNLWGHEFRSHH	133
Db	71	GQY EYYKVYMDKQDQADRCTIKKENTPLLNCAPKDQDIKFTIKFQEFSPNLWGLEFQKNK	130
QY	134	DYYIIATSDGTREGLES LQGGVCLTRGMKVLLRVGQ---SPRGGAVPRKPVSEMPMER-DR	190
Db	131	DYYIIISTSNGLSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSTRNKDPTRRPELEAGTN	190
QY	191	GAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC	250
Db	191	GRSSTTSFVKPNPGSSTDGNSAGHSGNNILGSEVALFAGIASGCIIFIVIIITLVLLL	250
QY	251	WRRRRRAKPSESRHPGPGSFGRGGS LGLGGGGMGPREAEPGELGIALRGGGAADPPFCPH	310
Db	251	KYRRRRHRKHSPQHTTTLSTLSTLATPKRSGNN---NGSEPSDIIPLR---TADSVFCPH	303
QY	311	YEKVSGDYGHPVYIVQDGPQSPNIIYKV	340
Db	304	YEKVSGDYGHPVYIVQEMPPQSPANIYKV	333

RESULT 6

EFB1_CHICK

ID EFB1_CHICK STANDARD; PRT; 334 AA.
AC 073612;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Ephrin-B1 precursor (CEK5 ligand) (CEL5-L).
GN EFNBL.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97223524; PubMed=9070326;
RA Holash J.A., Soans C., Chong L.D., Shao H., Dixit V.M.,
RA Pasquale E.B.;
RT "Reciprocal expression of the Eph receptor Cek5 and its ligand(s) in
RT the early retina."
RL Dev. Biol. 182:256-269(1997).
CC -!- SUBUNIT: Binds to the receptor tyrosine kinase EPHB2.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- PTM: Inducible phosphorylation of tyrosine residues in the
CC cytoplasmic domain (By similarity).
CC -!- SIMILARITY: Belongs to the ephrin family.
CC -----
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CC -----
DR EMBL; U72394; AAC07986.1; -.
DR InterPro; IPR008972; Cupredoxin.
DR InterPro; IPR001799; Ephrin.
DR Pfam; PF00812; Ephrin; 1.
DR PRINTS; PR01347; EPHRIN.
DR ProDom; PD002533; Ephrin; 1.
DR PROSITE; PS01299; EPHRIN; 1.
KW Developmental protein; Neurogenesis; Transmembrane; Glycoprotein;
KW Signal; Phosphorylation.
FT SIGNAL 1 25 POTENTIAL.
FT CHAIN 26 334 EPHRIN-B1.
FT DOMAIN 26 231 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 232 252 POTENTIAL.
FT DOMAIN 253 334 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 332 334 PDZ RECOGNITION MOTIF (POTENTIAL).
FT DISULFID 60 97 BY SIMILARITY.
FT DISULFID 85 149 BY SIMILARITY.
FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 334 AA; 36858 MW; 48AF556E9ED56CD5 CRC64;

Query Match

33.9%; Score 628; DB 1; Length 334;

Best Local Similarity 39.7%; Pred. No. 7.7e-34;
Matches 146; Conservative 50; Mismatches 100; Indels 72; Gaps 13;

```

Qy      8 PGGVR--VGALLLLGLVGLVSGLSLEPVYWNSANKRFQAEAGGYVLYPQIGDRLDLLCPRA 65
      | | | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      4 PRGGRWLLGVLLALCRLAAPLAKSLEPVSWWSAGNPKFMSGKGLVIYPEIGDKLDIICPKA 63

Qy     66 RPPGPHSSPNYEFYKLYLVGGAQGRRCCEAPPAPNLLLTCDRDLRLFTIKFQEYSPNLW 125
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     64 EPSKP-----YDYYKLYLVKKDQADACSTVMDPNVLVTCNRPEQEIRFTIKFQEFSPNYM 118

Qy    126 GHEFRSHHDYIIATSDGTREGLESLOGGVCLTRGMKVLLRVGQSPRGGAIVPRKPVSEMP 185
      | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | |
Db    119 GLEFKRQQDYFITSTSNGLDLENREGGVCQTRSMKIVMKVGQDP-NAVIPEQLTTSRP 177

Qy    186 MER-----DRGAAHSL----EPGKENLPGDPTSNA--TSRGAEGPLPPPSMPAVAGA 231
      : | | : | | | | | | | | | | | | | | | | | | | | | |
Db    178 SKEADNTVKIVTQSPRHVKVPTVEEPGK---PGSVNQNGQETQGPDSGFL--SSKVAVFAA 232

Qy    232 AGG-----LALLLLGVAGAGGAMCWRRRRRAKPSESRH-----PGPGSFGRG 272
      | | | | | | | | | | | | | | | | | | | | | | | | |
Db    233 IGAGCVIFILIIIFLVLLIKI-----RKRHRKHTQQRAAALSSTLASPKCSGNA 283

Qy    273 GSLGLGGGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQS 332
      || | | | | | | | | | | | | | | | | | | | | | | |
Db    284 GS-----EPSDIIIPLR---TTENNYCPHYEKVSGDYGHPVYIVQEMPPQS 326

Qy    333 PPNIYYKV 340
      | | | | | |
Db    327 PANIYYKV 334

```

RESULT 7

EFB2_BRARE

```

ID   EFB2_BRARE          STANDARD;          PRT;   332 AA.
AC   073874;
DT   15-JUL-1999 (Rel. 38, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Ephrin-B2 precursor (Ephrin B2a).
GN   EFNB2 OR EFNB2A.
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98438455; PubMed=9765210;
RA   Durbin L., Brennan C., Shiomi K., Cooke J., Barrios A.,
RA   Shanmugalingam S., Guthrie B., Lindberg R., Holder N.;
RT   "Eph signaling is required for segmentation and differentiation of
RT   the somites.";
RL   Genes Dev. 12:3096-3109(1998).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21290827; PubMed=11397014;

```

RA Chan J., Mably J.D., Serluca F.C., Chen J.N., Goldstein N.B.,
 RA Thomas M.C., Cleary J.A., Brennan C., Fishman M.C., Roberts T.M.;
 RT "Morphogenesis of prechordal plate and notochord requires intact
 RT eph/ephrin b signaling.";
 RL Dev. Biol. 234:470-482(2001).
 CC -!- SUBUNIT: Binds to the receptor tyrosine kinase EPHB4.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- PTM: Inducible phosphorylation of tyrosine residues in the
 CC cytoplasmic domain (By similarity).
 CC -!- SIMILARITY: Belongs to the ephrin family.
 CC -----
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 CC -----
 DR EMBL; AJ004863; CAA06168.1; -.
 DR EMBL; AF375225; AAK64275.1; -.
 DR ZFIN; ZDB-GENE-990415-67; efnb2a.
 DR InterPro; IPR008972; Cupredoxin.
 DR InterPro; IPR001799; Ephrin.
 DR Pfam; PF00812; Ephrin; 1.
 DR PRINTS; PR01347; EPHRIN.
 DR ProDom; PD002533; Ephrin; 1.
 DR PROSITE; PS01299; EPHRIN; 1.
 KW Developmental protein; Neurogenesis; Transmembrane; Glycoprotein;
 KW Signal; Phosphorylation.
 FT SIGNAL 1 24 POTENTIAL.
 FT CHAIN 25 332 EPHRIN-B2.
 FT DOMAIN 25 225 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 226 246 POTENTIAL.
 FT DOMAIN 247 332 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 330 332 PDZ RECOGNITION MOTIF (POTENTIAL).
 FT DISULFID 59 98 BY SIMILARITY.
 FT DISULFID 86 150 BY SIMILARITY.
 FT CARBOHYD 20 20 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 33 33 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 211 211 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 332 AA; 36724 MW; 189ED82372C71C8B CRC64;

Query Match 33.9%; Score 626.5; DB 1; Length 332;
 Best Local Similarity 42.2%; Pred. No. 9.6e-34;
 Matches 145; Conservative 54; Mismatches 106; Indels 39; Gaps 12;

QY 14 GALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLLCPRARPPGPHSS 73
 | |:: : | | : :||: | : | | | | | |:::|:| | |
 Db 11 GVLVIACKVNLSRALILDSIYWNTTNTKFPVGGQLVLYPQIGDKMDIVCPRVE---GGSM 67
 QY 74 PNYEFYKLYLVGGAQGRCEAPPAPNLLLTCDRDLRFTIKFQEYSPNLWGHEFRSHH 133
 |:| |::| | : | : | | | :| |::|:| | | | | | | |
 Db 68 EGVEYYKLYMVPLEQLKSCQVTKADTPLLNCVKPDQVKFTLKFQEFSPNLWGLEFFRGK 127
 QY 134 DYYIIATSDGTREGLES LQGGVCLTRGMKVLLRVGQSPRGGAVPRK-PVSEMPMERDRGA 192


```

Db      128 DYYIISTSNGTMEGLDNQEGGVCKTKSMKIIMKVGQNPSDPISPKDYPTSYPPKHPDLGG 187
QY      193 AHS-----LEP-----GKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGV 242
      |      |::|      |::|      |::|      |::|      |::|      |::|      |::|      |::|
Db      188 KDSKSNEVLKPDASPHGEDK--GDGNKSSSVIGSEVAL----FACIASASVIVIIIIIML 241
      :      :      :      :      :      :      :      :      :      :      :      :
QY      243 AGAGGAMCWRRRRRAKPSRHPGPGSFG-----RGGSLGLGGGGMGPREAEPGELGIA 296
      :      :      :      :      :      :      :      :      :      :      :      :
Db      242 VFL--LLKYRRRHRKHS-PQHATTLSLSTLATPKRGGS----GGNNNG---SEPSDIIIP 291
      :      :      :      :      :      :      :      :      :      :      :      :
QY      297 LRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIIYKV 340
      ||      ||      |||||      |||||      |||||      |||||      |||||      |||||
Db      292 LR---TADSVFCPHYEKVSGDYGHPVYIVQEMPQPSPANIYKV 332

```

RESULT 8

EFB1_MOUSE

```

ID      EFB1_MOUSE      STANDARD;      PRT;      345 AA.
AC      P52795;
DT      01-OCT-1996 (Rel. 34, Created)
DT      01-OCT-1996 (Rel. 34, Last sequence update)
DT      15-MAR-2004 (Rel. 43, Last annotation update)
DE      Ephrin-B1 precursor (EPH-related receptor tyrosine kinase ligand 2)
DE      (LERK-2) (ELK ligand) (ELK-L) (STRA1 protein) (CEK5 receptor ligand)
DE      (CEK5-L).
GN      EFNBI OR EPLG2 OR LERK2 OR STRA1 OR EPL2.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=129/Sv;
RX      MEDLINE=95203867; PubMed=7896266;
RA      Fletcher F.A., Renshaw B., Hollingsworth T., Baum P., Lyman S.D.,
RA      Jenkins N.A., Gilbert D.J., Copeland N.G., Davison B.L.;
RT      "Genomic organization and chromosomal localization of mouse Eplg2, a
RT      gene encoding a binding protein for the receptor tyrosine kinase
RT      elk.";
RL      Genomics 24:127-132(1994).
RN      [2]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=95377533; PubMed=7649373;
RA      Bouillet P., Oulad-Abdelghani M., Vicaire S., Garnier J.M.,
RA      Schunbaur B., Dolle P., Chambon P.;
RT      "Efficient cloning of cDNAs of retinoic acid-responsive genes in P19
RT      embryonal carcinoma cells and characterization of a novel mouse gene,
RT      Stra1 (mouse LERK-2/Eplg2).";
RL      Dev. Biol. 170:420-433(1995).
RN      [3]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Brain;
RX      MEDLINE=95014510; PubMed=7929389;
RA      Shao H., Lou L., Pandey A., Pasquale E.B., Dixit V.M.;
RT      "cDNA cloning and characterization of a ligand for the Cek5 receptor
RT      protein-tyrosine kinase.";

```

RL J. Biol. Chem. 269:26606-26609(1994).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Mammary gland;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RP FUNCTION.
 RX MEDLINE=20171264; PubMed=10704386;
 RA Imondi R., Wideman C., Kaprielian Z.;
 RT "Complementary expression of transmembrane ephrins and their receptors
 RT in the mouse spinal cord: a possible role in constraining the
 RT orientation of longitudinally projecting axons.";
 RL Development 127:1397-1410(2000).
 CC -!- FUNCTION: Binds to the receptor tyrosine kinases EPHB1 and EPHA1.
 CC Binds to, and induce the collapse of, commissural axons/growth
 CC cones in vitro. May play a role in constraining the orientation of
 CC longitudinally projecting axons.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- TISSUE SPECIFICITY: Expressed on lateral floor plate cells,
 CC specifically on commissural axon segments that have passed through
 CC the floor plate. Expressed in cells of the retinal ganglion cell
 CC layer during retinal axon guidance to the optic disc.
 CC -!- DEVELOPMENTAL STAGE: Expressed in the floor plate throughout the
 CC period of commissural axon pathfinding.
 CC -!- PTM: Inducible phosphorylation of tyrosine residues in the
 CC cytoplasmic domain.
 CC -!- SIMILARITY: Belongs to the ephrin family.
 CC -----
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 CC -----
 DR EMBL; U07602; AAC53247.1; -.

QY 340 V 340
|
Db 345 V 345

RESULT 9

EFB1_RAT

ID EFB1_RAT STANDARD; PRT; 345 AA.
AC P52796;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Ephrin-B1 precursor (EPH-related receptor tyrosine kinase ligand 2)
DE (LERK-2) (ELK ligand) (ELK-L).
GN EFNBI OR EPLG2 OR LERK2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=95022634; PubMed=7936648;
RA Fletcher F.A., Carpenter M., Shilling H., Baum P., Ziegler S.,
RA Gimpel S., Hollingsworth T., Vanden Bos T., Davison B.L.,
RA Lyman S.D., Beckmann M.P.;
RT "LERK-2, a binding protein for the receptor-tyrosine kinase ELK, is
RT evolutionarily conserved and expressed in a developmentally regulated
RT pattern.";
RL Oncogene 9:3241-3248(1994).
CC -!- FUNCTION: Binds to the receptor tyrosine kinases EPHB3
CC (preferred), EPHB1 and EPHA1. Binds to, and induce the collapse
CC of, commissural axons/growth cones in vitro. May play a role in
CC constraining the orientation of longitudinally projecting axons
CC (By similarity).
CC -!- SUBUNIT: Binds to the receptor tyrosine kinases EPHB3 (preferred),
CC EPHB1 and EPHB2.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- PTM: Inducible phosphorylation of tyrosine residues in the
CC cytoplasmic domain (By similarity).
CC -!- SIMILARITY: Belongs to the ephrin family.
CC -----
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CC -----
DR EMBL; U07560; AAA53092.1; -.
DR PIR; I58406; I58406.
DR InterPro; IPR008972; Cupredoxin.
DR InterPro; IPR001799; Ephrin.
DR Pfam; PF00812; Ephrin; 1.
DR PRINTS; PR01347; EPHRIN.

GN EFN1 OR EPLG2 OR LERK2.
 OS *Xenopus laevis* (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
 OC Xenopodinae; *Xenopus*.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97316777; PubMed=9174051;
 RA Jones T.L., Karavanova I., Chong L., Zhou R.P., Daar I.O.;
 RT "Identification of XLERK, an Eph family ligand regulated during
 RT mesoderm induction and neurogenesis in *Xenopus laevis*.";
 RL Oncogene 14:2159-2166(1997).
 CC -!- FUNCTION: May have a role in the developing mesenchymal and
 CC nervous tissue.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- TISSUE SPECIFICITY: In the adult, expressed at low levels in most
 CC adult tissues with increased levels observed in the kidney,
 CC oocytes, ovary and testis.
 CC -!- PTM: Inducible phosphorylation of tyrosine residues in the
 CC cytoplasmic domain (By similarity).
 CC -!- SIMILARITY: Belongs to the ephrin family.
 CC -----
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 CC -----
 DR EMBL; U31427; AAC35995.1; -.
 DR InterPro; IPR008972; Cupredoxin.
 DR InterPro; IPR001799; Ephrin.
 DR Pfam; PF00812; Ephrin; 1.
 DR PRINTS; PR01347; EPHRIN.
 DR ProDom; PD002533; Ephrin; 1.
 DR PROSITE; PS01299; EPHRIN; 1.
 KW Developmental protein; Neurogenesis; Transmembrane; Glycoprotein;
 KW Signal; Phosphorylation.
 FT SIGNAL 1 20 POTENTIAL.
 FT CHAIN 21 327 EPHRIN-B1.
 FT DOMAIN 21 225 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 226 246 POTENTIAL.
 FT DOMAIN 247 327 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 325 327 PDZ RECOGNITION MOTIF (POTENTIAL).
 FT DISULFID 57 93 BY SIMILARITY.
 FT DISULFID 81 145 BY SIMILARITY.
 FT CARBOHYD 131 131 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 202 202 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 327 AA; 36621 MW; 71230CE7F6BE5974 CRC64;

 Query Match 32.4%; Score 600; DB 1; Length 327;
 Best Local Similarity 39.8%; Pred. No. 4.8e-32;
 Matches 146; Conservative 43; Mismatches 100; Indels 78; Gaps 12;

 QY 10 GVR--VGALLLLGVLGLVSGLSLEPVYWSANKRFQAEAGGYVLYPQIGDRLDLLCPRA-- 65

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      |:| :| ||:| | :||| ||| | | : | |||:|||||:|:|:
Db      3 GLRRLGLLLVLYRLCSALGKNLEPVTWNSQNPRFISGKGLVLYPEIGDRLDIICPKGLF 62
QY      66 RPPGPHSSPNYEFYKLYLVGGAQGRRCAPPAPNLLTCDRDLRFTIKFQEYSPNLW 125
      :| ||:||||:| | | ||:|:|:| : |||:|:|:|
Db      63 QP-----YEYKLYMVRRDQLEACSTVIDPNVLVTCNQPGKEYRFTIKFQEFSPNYM 114
QY      126 GHEFRSHHDYIIATSDGTREGLESQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMP 185
      | ||| : ||| :||: | :||: :||| | | |:|:|:| | | | : :
Db      115 GLEFRRNQDYIITSTSNSTLQGLNREGGVCQTRSMKIIMKVGQDP--NAVPEQLT--- 169
QY      186 MERDRGAAHSLEPGKENLPGDPTSNAATSRGA-EGPLPPP-----SMPAVAGAAGGLA 236
      : | || | | : | ||: | | | | |
Db      170 -----TTRPSKE---ADNTGKIATFGPWNGPVQNPGKSDTNLSDKPTGRWGVGDF 217
QY      237 LLLGLVAGAGGAMC-----WRRRRRAKPSE-----SRHPGPGSFGRGG 273
      : | | || | | | | | | | | | | | | | | | | | |
Db      218 NSKIAVFAAIGAGCVIFILIIIFLVLLIKIRKHKHTQQAALSLSTLASPKCSGNAG 277
QY      274 SLGLGGGGMGMPREAPGELGIALRGGAADPPFCPHYEKVSGDYGHPVYIVQDGPQSP 333
      | | | | | | | | | | | | | | | | | | | | | |
Db      278 S-----EPSDIIIPLR---TTENNYCPHYEKVSGDYGHPVYIVQEMPPQSP 320
QY      334 PNIYYKV 340
      |||||
Db      321 ANIYYKV 327

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RESULT 11

EFA2_BRARE

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ID   EFA2_BRARE          STANDARD;          PRT;   195 AA.
AC   P79727;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Ephrin-A2 precursor (EPH-related receptor tyrosine kinase ligand 6)
DE   (LERK-6) (ELF-1) (ZFEPHL3).
GN   EFNA2 OR EPLG6 OR LERK6.
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryo;
RX   MEDLINE=97195707; PubMed=9043080;
RA   Brennan C., Monschau B., Lindberg R., Guthrie B., Drescher U.,
RA   Bonhoeffer F., Holder N.;
RT   "Two Eph receptor tyrosine kinase ligands control axon growth and may
RT   be involved in the creation of the retinotectal map in the
RT   zebrafish.";
RL   Development 124:655-664(1997).
CC   -!- FUNCTION: Control axon growth and may be involved in the creation
CC   of the retino-tectal map.
CC   -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
CC   (Potential).

```

CC -!- TISSUE SPECIFICITY: Widespread expression in the embryo.
 CC -!- DEVELOPMENTAL STAGE: Expressed in the presumptive midbrain of
 CC developing embryos from the six-somite stage. By 24 hours,
 CC expressed throughout the midbrain including the region of the
 CC presumptive tectum. At later stages, expressed in a graded fashion
 CC throughout the tectum.
 CC -!- SIMILARITY: Belongs to the ephrin family.

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 CC -----

DR EMBL; Y09668; CAA70863.1; -.
 DR ZFIN; ZDB-GENE-990415-66; efna2.
 DR InterPro; IPR008972; Cupredoxin.
 DR InterPro; IPR001799; Ephrin.
 DR Pfam; PF00812; Ephrin; 1.
 DR PRINTS; PR01347; EPHRIN.
 DR ProDom; PD002533; Ephrin; 1.
 DR PROSITE; PS01299; EPHRIN; 1.
 KW Developmental protein; Neurogenesis; Glycoprotein; Lipoprotein;
 KW Membrane; GPI-anchor; Signal.
 FT SIGNAL 1 16 POTENTIAL.
 FT CHAIN 17 174 EPHRIN-A2.
 FT PROPEP 175 195 REMOVED IN MATURE FORM (POTENTIAL).
 FT DISULFID 57 97 BY SIMILARITY.
 FT LIPID 174 174 GPI-anchor amidated cysteine (Potential).
 FT CARBOHYD 32 32 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 195 AA; 22688 MW; 9EE284FEB61D0C42 CRC64;

Query Match 10.0%; Score 185; DB 1; Length 195;
 Best Local Similarity 29.9%; Pred. No. 1.6e-05;
 Matches 63; Conservative 21; Mismatches 71; Indels 56; Gaps 7;

QY 33 VYWN SANKRFQ AEGGYVLPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVGGAQGRRC 92
 ||||:| || :| | : | | | : | | | | | | :| |
 Db 29 VYWNSSNSRFW-QGEYTVAVSINDYLDVYCPYYESPQPHS--RMERYILFMVNHDGYLTC 85
 QY 93 EAPPAPNLLLTCDR---PDLDLRFTIKFQEYSPNLWGHEFRSHHDYIIATSDGTREGLE 149
 | :| | | | | :| | | | | :| | | | | :| | | |
 Db 86 EHRMRGFKRWE CNRPQSPDGPLRFSEKFQLF TPFSLGFEFRPGHEYYYISSPHPNHAGKP 145
 QY 150 SLQGGVCLTRGMKVLLRVGQSPRGGA VPRKPVSEMPMERDRGA AHSLEPGKENLPGDPTS 209
 | : :| | : | | | | | | | :| | |
 Db 146 CLK-----LKVYV-----KPTSS-----GYESPEPFLTD 169
 QY 210 NATSRGAEGPLPPPSMPAVAGAAGGLALLL 240
 : ||:| | | | :| | :| |
 Db 170 QSQR CGADGPC-----LAVLML 186

RESULT 12
 EFA3_HUMAN

ID EFA3_HUMAN STANDARD; PRT; 238 AA.
 AC P52797;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Ephrin-A3 precursor (EPH-related receptor tyrosine kinase ligand 3)
 DE (LERK-3) (EHK1 ligand) (EHK1-L).
 GN EFNA3 OR EPLG3 OR LERK3 OR EFL2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95140419; PubMed=7838529;
 RA Kozlosky C.J., Maraskovsky E., McGrew J.T., Vanden Bos T.,
 RA Teepe M., Lyman S.D., Srinivasan S., Fletcher F.A., Gayle R.B. III,
 RA Cerretti D.P., Beckmann M.P.;
 RT "Ligands for the receptor tyrosine kinases hek and elk: isolation of
 RT cDNAs encoding a family of proteins.";
 RL Oncogene 10:299-306(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95063919; PubMed=7973638;
 RA Davis S., Gale N.W., Aldrich T.H., Maisonpierre P.C., Lhotak V.,
 RA Pawson T., Goldfarb M., Yancopoulos G.D.;
 RT "Ligands for EPH-related receptor tyrosine kinases that require
 RT membrane attachment or clustering for activity.";
 RL Science 266:816-819(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Duodenum;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
 CC -!- TISSUE SPECIFICITY: Expressed in brain, skeletal muscle, spleen,
 CC thymus, prostate, testis, ovary, small intestine, and peripheral
 CC blood leukocytes.

CC -!- SIMILARITY: Belongs to the ephrin family.
CC -----
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CC -----
DR EMBL; U14187; AAC50078.1; -.
DR EMBL; L37360; AAA52368.1; -.
DR EMBL; BC017722; AAH17722.1; -.
DR PIR; I38849; I38849.
DR Genew; HGNC:3223; EFNA3.
DR MIM; 601381; -.
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0005005; F:transmembrane-ephrin receptor activity; TAS.
DR GO; GO:0007267; P:cell-cell signaling; TAS.
DR InterPro; IPR008972; Cupredoxin.
DR InterPro; IPR001799; Ephrin.
DR Pfam; PF00812; Ephrin; 1.
DR PRINTS; PR01347; EPHRIN.
DR ProDom; PD002533; Ephrin; 1.
DR PROSITE; PS01299; EPHRIN; 1.
KW Glycoprotein; Lipoprotein; Membrane; GPI-anchor; Signal.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 214 EPHRIN-A3.
FT PROPEP 215 238 REMOVED IN MATURE FORM (POTENTIAL).
FT DISULFID 63 110 BY SIMILARITY.
FT LIPID 214 214 GPI-anchor amidated glycine (Potential).
FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 67 67 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 71 74 MISSING (IN REF. 2).
SQ SEQUENCE 238 AA; 26350 MW; 8EFD6AE8FE33FD DA CRC64;

Query Match 9.7%; Score 179; DB 1; Length 238;
Best Local Similarity 28.4%; Pred. No. 4.8e-05;
Matches 65; Conservative 24; Mismatches 80; Indels 60; Gaps 12;

Qy 7 GPGGVRVGALLLLGLVGLVSGLSLEPVYWN SANKRFQAE GGYVLYPQIGDRLDLLCP--R 64
 | | | | | | : | | | | : : : | | | : : | | | : |
Db 24 GPG-----GALG-----NRHAVYWNSSNQHLRRE-GYTVQVNVNDYLDIYCPHYN 67
Qy 65 ARPGPHSSP----NYEFYKLYLVGGAQGRRC EAPPAPNLLLTCDR PDL---DLRFTIKF 117
 : | | : | | | | | : | | | | | : | | : : : | |
Db 68 SSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQGFK-RWECNRPHAPHSP IKFSEKF 126
Qy 118 QEYSPNLWGHEFRSHHDYIIATSDGTREGLES LQGGVCLTRGMKVLLRVGQSPRGGA VP 177
 | | | | : | | : | : | | | : | | | | | | : : |
Db 127 QRYSAFSLGYEFHAGHEYYYYISTPTHNLH-----WKCLR--MKVFVCCASTSHSG--- 174
Qy 178 RKPVSEMP-----MERDRGAHSLE-----PGKENLP 204
 | | | : | | : | | | : | : | |
Db 175 EKPVPTLPQFTMGPNVKINVLEDFEGENPQVPKLEKSISGTSPKREHLP 223

RESULT 13

EFA2_MOUSE

ID EFA2_MOUSE STANDARD; PRT; 209 AA.
AC P52801;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Ephrin-A2 precursor (EPH-related receptor tyrosine kinase ligand 6)
DE (LERK-6) (ELF-1) (CEK7-ligand) (CEK7-L).
GN EFNA2 OR EPLG6 OR LERK6 OR ELF1 OR EPL6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Swiss Webster; TISSUE=Brain;
RX MEDLINE=95007776; PubMed=7522971;
RA Cheng H.J., Flanagan J.G.;
RT "Identification and cloning of ELF-1, a developmentally expressed
RT ligand for the Mek4 and Sek receptor tyrosine kinases.";
RL Cell 79:157-168(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=95181289; PubMed=7876076;
RA Shao H., Lou L., Pandey A., Verderame M.F., Siever D.A., Dixit V.M.;
RT "cDNA cloning and characterization of a Cek7 receptor
RT protein-tyrosine kinase ligand that is identical to the ligand
RT (ELF-1) for the Mek-4 and Sek receptor protein-tyrosine kinases.";
RL J. Biol. Chem. 270:3467-3470(1995).
CC -!- SUBUNIT: Binds to the receptor tyrosine kinases EPHA3, EPHA4 and
CC EPHA5.
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
CC (Potential).
CC -!- SIMILARITY: Belongs to the ephrin family.
CC -----
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CC -----
DR EMBL; U14941; AAA53636.1; -.
DR EMBL; U14752; AAA68520.1; -.
DR PIR; A54984; A54984.
DR MGD; MGI:102707; Efna2.
DR InterPro; IPR008972; Cupredoxin.
DR InterPro; IPR001799; Ephrin.
DR Pfam; PF00812; Ephrin; 1.
DR PRINTS; PR01347; EPHRIN.
DR ProDom; PD002533; Ephrin; 1.
DR PROSITE; PS01299; EPHRIN; 1.
KW Glycoprotein; Lipoprotein; Membrane; GPI-anchor; Signal.

FT	SIGNAL	1	20	POTENTIAL.
FT	CHAIN	21	184	EPHRIN-A2.
FT	PROPEP	185	209	REMOVED IN MATURE FORM (POTENTIAL).
FT	DISULFID	69	110	BY SIMILARITY.
FT	LIPID	184	184	GPI-anchor amidated asparagine
FT				(Potential).
FT	CARBOHYD	38	38	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	170	170	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	184	184	N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ	SEQUENCE	209 AA; 23586 MW; F1997545F25B9ABC CRC64;		

Query Match 9.5%; Score 176; DB 1; Length 209;
 Best Local Similarity 29.3%; Pred. No. 6.6e-05;
 Matches 58; Conservative 19; Mismatches 69; Indels 52; Gaps 7;

Qy	33	VYWNSANKRFQAE-----GGYVLYPQIGDRLLDLCPRARPPGPHSSPNYEFYKLYLVGGA	87
		: : : : : :	
Db	35	VYWNRSNPRFQVSAVGDDGGGYTVEVSINDYLDIYCPHYGAPLP-PAERMERYILYMVNGE	93
Qy	88	QGRRCCEAPPAPNLLLTCDRDL---DLRFTIKFQEYSPNLWGHEFRSHHDYIIATSDGT	144
		: : : : : : : : :	
Db	94	GHASCDHRQRGFKRWEENRPAAPGGPLKFSEKFQLETFPSLGFEEFRPGHEYYYYISATP--	151
Qy	145	REGLESIQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGAAHSLEPGKENLP	204
		: : :	
Db	152	----PNLVDRPCLR--LKVVYVR-----PTNETLY	174
Qy	205	GDP----TSNATSRGAEG	218
		:	
Db	175	EAPEPIFTSNSSCSGLGG	192

RESULT 14

EFA2_HUMAN

ID EFA2_HUMAN STANDARD; PRT; 213 AA.
 AC O43921; O76020;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Ephrin-A2 precursor (EPH-related receptor tyrosine kinase ligand 6)
 DE (LERK-6) (HEK7-ligand) (HEK7-L).
 GN EFNA2 OR EPLG6 OR LERK6.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 GN NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98126446; PubMed=9465306;
 RA Cerretti D.P., Nelson N.;
 RT "Characterization of the genes for mouse LERK-3/Ephrin-A3 (Epl3),
 RT mouse LERK-4/Ephrin-A4 (Epl4), and human LERK-6/Ephrin-A2 (EPLG6):
 RT conservation of intron/exon structure."
 RL Genomics 47:131-135(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Lamerdin J.E., McCready P.M., Skowronski E., Adamson A.W.,

RA Burkhart-Schultz K., Gordon L., Kyle A., Ramirez M., Stilwagen S.,
 RA Phan H., Velasco N., Garnes J., Danganan L., Poundstone P.,
 RA Christensen M., Georgescu A., Avila J., Liu S., Attix C., Andreise T.,
 RA Trankheim M., Amico-Keller G., Coefield J., Duarte S., Lucas S.,
 RA Bruce R., Thomas P., Quan G., Kronmiller B., Arellano A.,
 RA Montgomery M., Ow D., Nolan M., Trong S., Kobayashi A., Olsen A.O.,
 RA Carrano A.V.;
 RL Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=99045414; PubMed=9826538;
 RA Aasheim H.C., Pedetour F., Grosgeorge J., Logtenberg T.;
 RT "Cloning, chromosomal mapping, and tissue expression of the gene
 RT encoding the human Eph-family kinase ligand ephrin-A2.";
 RL Biochem. Biophys. Res. Commun. 252:378-382(1998).
 CC -!- SUBUNIT: Binds to the receptor tyrosine kinases EPHA3, EPHA4 and
 CC EPHA5.
 CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
 CC (Potential).
 CC -!- SIMILARITY: Belongs to the ephrin family.
 CC -----
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 CC -----
 DR EMBL; U92896; AAC39577.1; -.
 DR EMBL; U92893; AAC39577.1; JOINED.
 DR EMBL; U92894; AAC39577.1; JOINED.
 DR EMBL; AC004258; AAC04896.1; -.
 DR EMBL; AJ007292; CAA07435.1; -.
 DR PIR; JE0322; JE0322.
 DR Genew; HGNC:3222; EFNA2.
 DR MIM; 602756; -.
 DR GO; GO:0005106; F:ephrin; TAS.
 DR GO; GO:0007267; P:cell-cell signaling; TAS.
 DR InterPro; IPR008972; Cupredoxin.
 DR InterPro; IPR001799; Ephrin.
 DR Pfam; PF00812; Ephrin; 1.
 DR PRINTS; PR01347; EPHRIN.
 DR ProDom; PD002533; Ephrin; 1.
 DR PROSITE; PS01299; EPHRIN; 1.
 KW Glycoprotein; Lipoprotein; Membrane; GPI-anchor; Signal.
 FT SIGNAL 1 24 POTENTIAL.
 FT CHAIN 25 188 EPHRIN-A2.
 FT PROPEP 189 213 REMOVED IN MATURE FORM (POTENTIAL).
 FT DISULFID 73 114 BY SIMILARITY.
 FT LIPID 188 188 GPI-anchor amidated asparagine
 FT (Potential).
 FT CARBOHYD 42 42 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 174 174 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 188 188 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 6 6 R -> A (IN REF. 3).

FT CONFLICT 25 26 RA -> PP (IN REF. 3).
 FT CONFLICT 29 30 AA -> RR (IN REF. 3).
 SQ SEQUENCE 213 AA; 23878 MW; 33C9FB1A8168B2D0 CRC64;

Query Match 9.5%; Score 175.5; DB 1; Length 213;
 Best Local Similarity 36.8%; Pred. No. 7.2e-05;
 Matches 43; Conservative 14; Mismatches 51; Indels 9; Gaps 3;

Qy 33 VYWSANKRFQA-----EGGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVGGA 87
 |||| :| || | ||| : | | || :| | | : | | || :| |
 Db 39 VYWNRSNPRFHAGAGDDGGGYTVEVSINDYLDIYCPHYGAPLP-PAERMEHYVLYMVNGE 97
 Qy 88 QGRRCEAPPAPNLLLLTCDRPDL---DLRFTIKFQEYSPNLWGHEFRSHHDYIIATS 141
 |: ||| |:| :|| ||| :|| | ||| |:| | : :
 Db 98 GHASCDHRQRGFKRWECNRPAAPGGPLKFSEKFQLFTPFSLGFEPFRPGHEYYYYISAT 154

RESULT 15

EFA2_CHICK

ID EFA2_CHICK STANDARD; PRT; 200 AA.
 AC P52802;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Ephrin-A2 precursor (EPH-related receptor tyrosine kinase ligand 6)
 DE (LERK-6) (ELF-1).
 GN EFNA2 OR EPLG6 OR LERK6 OR ELF1.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95360981; PubMed=7634327;
 RA Cheng H.J., Nakamoto M., Bergemann A.D., Flanagan J.G.;
 RT "Complementary gradients in expression and binding of ELF-1 and Mek4
 in development of the topographic retinotectal projection map.";
 RL Cell 82:371-381(1995).
 CC -!- SUBUNIT: Binds to the receptor tyrosine kinases EPHA3, EPHA4 and
 CC EPHA5 (By similarity).
 CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
 CC (Potential).
 CC -!- TISSUE SPECIFICITY: Expressed in a gradient across the tectum
 CC being more strongly expressed at the posterior pole.
 CC -!- SIMILARITY: Belongs to the ephrin family.

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 CC -----

DR EMBL; L40932; AAC42229.1; -.
 DR InterPro; IPR008972; Cupredoxin.

DR InterPro; IPR001799; Ephrin.
 DR Pfam; PF00812; Ephrin; 1.
 DR PRINTS; PR01347; EPHRIN.
 DR ProDom; PD002533; Ephrin; 1.
 DR PROSITE; PS01299; EPHRIN; 1.
 KW Glycoprotein; Lipoprotein; Membrane; GPI-anchor; Signal.
 FT SIGNAL 1 22 POTENTIAL.
 FT CHAIN 23 175 EPHRIN-A2.
 FT PROPEP 176 200 REMOVED IN MATURE FORM (POTENTIAL).
 FT DISULFID 61 101 BY SIMILARITY.
 FT LIPID 175 175 GPI-anchor amidated asparagine
 FT (Potential).
 FT CARBOHYD 36 36 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 161 161 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 175 175 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 200 AA; 23049 MW; 8FAB1AE5E45EED96 CRC64;

Query Match 9.3%; Score 172; DB 1; Length 200;
 Best Local Similarity 35.3%; Pred. No. 0.00011;
 Matches 49; Conservative 16; Mismatches 58; Indels 16; Gaps 5;

Qy 15 ALLLLGLVGLVSGLSLEP-----VYWNSANKRFQAEGGYVLYPQIGDRDLDCPRA 65
 | || :| | | :| ||| :| || | | : | | || : ||
 Db 7 AALLAAIVG-VCVWSDDPGKVISDRYAVYWNRSNPRFH-RGDYTVSVSINDYLDIYCPHY 64

 Qy 66 RPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDL---DLRFTIKFQEYSP 122
 | | : | | || :| | : | :|| | :|| :|| :|| :||
 Db 65 EEPLP--AERMERYVLYMVNYEGHASCDRQKGFKRWECNRPDSPSGPLKFSEKFQLEFTP 122

 Qy 123 NLWGHEFRSHHDYIIATS 141
 | ||| | :|| | : |
 Db 123 FSLGFEFRPGHEYYSAS 141

Search completed: September 15, 2004, 12:36:31
 Job time : 14.2579 secs